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(54) Title: UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION

(57) Abstract: The invention provides novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin and a method for identification of the specific animal from a given biological sample.

UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION TECHNICAL FIELD

The invention relates to the identification of novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin at species and sub-species sources. The invention also provides a method for the identification of fragments on mitochondrial cytochrome b gene in biological material of unknown origin.

BACKGROUND ART

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A large number of studies in evolutionary biology utilize phylogenetic information obtained from mitochondrial cytochrome b gene. It has been identified a potent molecule to distinguish the phylogenetic depth of different lineages to family, genus and species in molecular taxonomy¹⁻⁶⁶. A vast database of the sequences of cytochrome b gene of different animal species has accumulated in public databases such as GenBank, NCBI (http://www.ncbi.nlm.nih.gov) etc. We have utilized this capacity of cytochrome b gene in establishing the identity of the origin of animal parts and product to its family, genus and species sources. The technique developed is based on a pair of universal primer that can amplify a small fragment of cytochrome b gene from a vast range of animal species. Establishing identity of confiscated animal parts and products is a great challenge to law enforcement agencies because none of the methods available till date is too efficient to reveal the identity of animal remains beyond a reasonable doubt. Morphological markers, described for certain species allow the identification of complete specimen of animals⁶⁷. However, a complete specimen is confiscated very rarely by the investigation agencies; therefore, these marker are not practical in wildlife forensics. The biochemical traits such as the bile characteristics⁶⁸ blood heam analysis^{69,70} etc. have also been employed in wildlife forensic for identification of individual species. The difficulty of these markers are that these markers are limited in number and are rarely found in their natural forms in which these were originally described as the characteristic of a particular species.

The molecular approaches such as micro-satellite based identification⁷¹, Restriction fragment length polymorphism analysis of mitochondrial genes or PCR based species specific STS markers require the prior information of the species to establish the identity^{72,73}. These methods also need a significant amount of DNA material to be analysed. We may not have the prior information about the species origin of confiscated animal parts and product in forensics, therefore, these methods are not really useful and

practical in wildlife identification. The technique invented by us is universal, therefore does not require any background information to establish the identity of any unknown confiscated remains at family, genus and species sources. Being a PCR based procedure it can be applied with trace amount of any biological material. Because the amplicon length is small (472 bp); therefore, it can work perfectly with the mutilated remains, which are commonly seized by the crime investigation agencies. It does not require the large amount of genetic material i.e. DNA to be analyzed to establish the identity, hence, can detect a minute amount of adulteration in food products. The procedure described is simple and very fast. Due to the said advantages, the procedure invented by us is most suited for forensic wildlife identification.

OBJECTS OF THE INVENTION

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The main object of the invention is to identify a fragment on mitochondrial cytochrome b gene capable of significantly discriminating among various evolutionary lineages of different animal species.

Another object is to identify a fragment on mitochondrial cytochrome b gene which is flanked by the highly conserved sequences at a vast range of animal species.

Yet another object is to detect a fragment on mitochondrial cytochrome b gene which is polymorphic inter-specifically, but monomorphic at intra species sources.

Still another object is to develop the universal primers to amplify the fragment on mitochondrial cytochrome b gene using polymerase chain reaction.

Another object is to develop a PCR protocol that works universally with DNA template of any unknown origin (i.e. all the animal species).

Yet another object is to provide a universal method for identification of species of analyzed material (i.e. the DNA isolated from confiscated animal remain of unknown origin) using the public databases such as GenBank, NCBI etc.

Still another object is to provide a universal method of animal identification to establish the crime with the criminal beyond a reasonably doubt.

Another object is provide a universal method to establish the identity of biological materials such as skin, horns etc confiscated from animal poachers, if it is that of an endangered species.

Yet another object is to provide a universal method for establishment of the identity of confiscated animal parts and products of endangered animal species for the purpose of production of molecular evidence of animal hunting and related crime in the court of law, so that the human violation to the wildlife resources could be controlled.

Still another object is to provide a universal technique to have an idea of the geographical location of the commitment of wildlife crime based on the haplotype of poached animal identified by the universal primer invented.

Another object is to provide a universal technique of animal identification to detect the adulteration of animal meat/products in vegetarian food product for the purpose of food fortification, by the food fortification agencies.

Yet another object is to provide a universal technique for detection of the origin of blood or blood stains etc collected from the scene of crime related to offences such as murder, rape etc, in order to establish the origin of blood found at scene of crime when it sounds as if criminals have wontedly spread the blood of an animal at the scene of crime, to confuse the crime investigation agencies and forensic scientists with human blood.

Another object is to invent and authenticate a universal technique that can be converted to a (a) 'MOLECUALR KIT' and (b) 'DNA CHIPS' based application to meet the requirements of above objectives.

15 SUMMARY OF THE INVENTION

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Accordingly, the invention provides novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin

DETAILED DESCRIPTION OF THE INVENTION

Keeping in view the above objectives, the cytochrome b gene sequences (1140 bp) of 221 distantly related animal species (listed in Table 1) representing various families were obtained from public database NCBI (http://www.ncbi.nlm.nih.gov). These sequences were aligned using the software Clustal X(1.8)(NCBI, USA) and a fragment (of 472 bp, alignment shown in Table 2) of gene was identified which had all the features mentioned above under column 1, 2 and 3 of sub-heading 'Objectives of invention'. As for the identity of this fragment we would like to mention that it includes the nucleotides between 398 to 869 in Antilope cervicapra and Felis catus; however, 399 to 870 in Homo sapiens sapiens species. Except at few positions (marked as star (*) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, giving rise to their unique molecular signature. These molecular signatures are characteristic of its species and form the basis of revealing the identity of the biological material of an unknown animal origin by the procedure invented by us. Considering Antilope cervicapra as a representative species, the sequence of this fragment is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of Antilope cervicapra:

"taccatgaggacaaatatctttttgaggagcaacagtcatcaccaatctcetttcagcaatcccatacatcggtacaaacctagtaga atgaatctgaggagggttctcagtagataaagcaacccttacccgatttttcgccttcactttatcctcccatttatcattgcagccett accatagtacacctactgtttctccacgaaacaggatccaacaaccccacaggaatctcatcagaacgcagacaaaattccattcaac ccctactacactatcaaagatatcctaggagctctactattaattttaaccctcatgcttctagtcctattctcaccggacctgcttggag acccagacaactatacaccagcaaacccacttaatacacccccacatatcaagccgaatgatacttcctatttgcatacgcaatcct ccgatcaattcctaacaaactaggagg".

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A pair of universal primer was designed to amplify this fragment in polymerase chain reaction (PCR). These primers were named as 'mcb398' and 'mcb869' because of its property to amplify a region of mitochondrial cytochrome b gene between nucleotides 398 to 869 of Antilope cervicapra, a representative animal species for this invention. We took this animal species as representative species because the idea of developing such a novel primers came in the mind of inventors while they were working on the genome of this animal in Centre for Cellular and Molecular Biology, Hyderabad, India. These primers work universally because its 3' end are highly conserved amongst a vast range of animal species (shown in Table 2). As mentioned above, the DNA fragment (sequence of which is shown above) targeted by these primers is highly polymorphic inter-specifically; however, it is monomorphic among the individual of same species (Tables 6, 7a, 7b, 7c, 1d and 8, respectively). These unique features of the targeted region enable these primers to generate the molecular signatures of an individual species; thereby, enabling them to differentiate amongst the animals of different species (see in Figure 1c). The variation within the fragment amplified by these primers increase with increasing distances of evolutionary lineages of two animals (Table 8). These unique features of the fragment amplified by the universal primers 'mcb398' and 'mcb869' invented by the applicants fulfill the objectives of invention.

Thus, the primers invented by us can generate the molecular signature from any biological material of unknown animal origin, which actually is the characteristic of its family, genus and more precisely, the species. When these signatures are compared in-silico with the signatures already available in public databases (viz., GenBank, NCBI database etc) using 'BLAST software⁷³, it indicates identity of the family, genus or species of the analyzed material, which in turn is confirmed practically by comparing with the reference animals of the revealed family, genus or species, by including them in the further analysis by the primers 'mcb398' and 'mcb869'. The complete procedure involved in the analyses (the word, 'analyses' should be understood with the stepwise procedure to establish the identity of the biological remain of any unknown animal origin for the aims mentioned in columns

1-13 under sub-heading 'Objectives of invention') is briefed under 'Examples 5 and 6, respectively, as well as illustrated in Figures 1a, 1b and 1c, respectively.

BRIEF DESCRIPTION OF DRAWING AND TABLES

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Figure 1a. Illustration of the step-wise procedure involved in *analyses*. The unknown biological material i.e. 'adil.flesh' refers to the confiscated skin mentioned in 'Example 6'. The arrow marks indicate the stepwise procedure involved. The brief description of Figure 1a is as follows:

The biological material i.e. the confiscated skin 'adil.flesh' was subjected to DNA isolation using the standard procedures⁷⁴. The DNA obtained was amplified using the primers 'mcb398' and 'mcb869' in PCR, fractionated in 2% (w/v) agarose gel, visualized and photographed under UV light using Gel Documentation System (Syngene, USA). The lane 'M' shown in the photograph represents the molecular weight marker (Marker XIII, Boehringer mannheim). Lane 1 shows the PCR amplicon (472 bp) obtained from 'adil.flesh' using primers 'mcb398' and 'mcb869'. The PCR amplicon obtained were sequenced at both the strand using "ABI Prism 3700 DNA Analyzes, PE-Applied Biosystems). The chromatogram shows the sequences (about 80 bp long, i.e. between 150-230 bp of sequence (328 bp), revealed from the PCR product of 472 bp length) obtained from 'adil.flesh'.

Figure 1b. Illustrates the further steps involved in analyses. The sequence (328 bp) revealed from 'adil.flesh' was subjected to homology search in nr (i.e. non-redundant) database of Netional Centre for Biological Information (NCBI), USA. The sequences producing significant alignments are shown along with its bits score and E values. It indicates the extent of homology amongst the sequence enquired (i.e. the 328 bp sequence from adil.flesh) and the sequences registered in nr database of NCBI. BLAST analysis revealed the highest homology of the sequence revealed from 'adil.flesh' with the sequence of Panthera pardus (gene bank registration number 'AY005809'), indicating the identity of adil.flesh as that of a leopard (Panthera pardus) origin. Figure 1b further illustrates the multiple alignments of the sequences obtained from reference animals (listed in Table 5) along with the sequence obtained from 'adil.flesh'. The sequences of 'adil.flesh' is similar to the sequences of 'gz1L' further confirming the identity of the source of confiscated remain 'adil.flesh' as that of a Panthera pardus origin.

Figure 1c illustrates the NJ-tree (Neighbor Joining tree) constructed using CLUSTAL X (1.8) from the sequences revealed from 'adil flesh' and reference animals listed in Table 5.

The animals belonging to similar species cluster together; however, the animals of different species group in different clusters. The confiscated material under investigation (i.e. 'adil.flesh') clusters with 'gz1L' (i.e. the known normal leopard 'Panthera pardus') indicating the identity of the species of 'adil.flesh' as that of a Panthera pardus source.

- Figure 2 shows the Agarose gel electrophorogram showing the PCR amplicons (472 bp) obtained from the reference animals of family felidae listed in Table 5, using universal primers 'mcb398 and 'mcb869'. Description of different lanes is as follows:
 - Lanes 1-21: The PCR profiles of the animals 1-21, respectively, listed in Table 5.
- Lane 22: The PCR profiles of DNA isolated from confiscated skin of unknown animal origin 'i.e. adil.flesh'
 - Lane 23: Negative control (no DNA)
 - Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)
 - Figure 3. Shows PCR amplicons obtained from animals listed in Table 9. The primers used in PCR are 'AFF' and 'AFR'. The description of different lanes shown is as follows:
- Lane 1-4: The PCR profiles of animals 1-4, respectively, listed in Table 9, showing amplicons of 354 bp.
 - Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)
 - Figure 4. Shows PCR amplicons obtained from animals listed in Table 12. This experiment demonstrates the universal nature of our primers among a vast range of animal species. Description of different lanes shown is as follows:
 - Lanes 1-23: The PCR profiles of the animals 1-23, respectively, listed in Table 12. The PCR product of 472 bp is amplified universally from all the animal species analyzed.
 - Lane 24: Negative control (no DNA)

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- Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)
- 25 **Table** 1. List of 221 animal species used for *In-silico* analysis to design the universal primers 'mcb398' and 'mcb869'. Table also demonstrate the 'P,S scores' of 'mcb398' and 'mcb869' for different templates. The descriptions of various symbols used in this table are as follows:
 - Symbol (#) refers to Number
- Symbol (*) refers to the animal species which is either protected species (listed in Wildlife (Protection) Act, 1972 (Central Act NO 53 of 1972), or an endangered/rare animal species Symbol (\$P,S/F) refers to Probability of match and Stability of match of primer 'mcb398' with different templates (i.e. the cytochrome b gene from different species origin). A higher P, S score refers to the higher probabilities of significant amplification of specific

template by the primer. It is calculated by Amplify (1.2) software.

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Symbol (${}^{\Psi}P,S/R$) refers to <u>Probability</u> of match and <u>Stability</u> of match of primer 'mcb869' with different templates. A higher P,S score refers to the higher probabilities of significant amplification of specific template by the primer. It is calculated by *Amplify* (1.2) software.

Table 2. Multiple sequence alignment of 472 bp fragment of mitochondrial cytochrome b gene (identified by inventors to fulfill the requirements of column 1, 2 and 3 mention under sub-heading 'Objectives of invention') of 221 animal species listed in Table 1. Alignments also show the binding sites for universal primers 'mcb398' and 'mcb869'. The symbol (*) refers to the nucleotide bases which are conserved amongst 221 animal species listed in Table 1). The alignments have been done using software CLUSTAL X (1.8). The nucleitide positions that are unmarked are variable amongst 221 animal species analyzed. These variable sites together constitute the molecular signature of an individual species, giving rise to molecular basis of species identification by our primers.

Table 3. Results of the blast analysis of the sequence revealed from 'adil.flesh' in 'mito' database of NCBI. It shows the most significant alignment of cytochrome b sequence (328 bp) revealed from confiscated skin piece 'adil.flesh' with felis catus cytochrome b gene sequence (genbank registration number NC_001700.1, bits score 365, E value, e-101) registered in NCBI database (bits score 365 and E value e-101). It gives an indication that the species of analyzed material belongs to family felidae. It also fulfills the requirements of column 6 mention above under sub-heading 'Objectives of invention'.

Table 4. Results of the blast analysis of the sequence revealed from 'adil.flesh' in 'nr' database of NCBI. It shows the most significant alignment of cytochrome b sequence (328 bp) revealed from confiscated skin piece 'adil.flesh' with Panthera pardus cytochrome b gene sequence (genbank registration number AY005809, bits score 603, E value, e-170) registered in NCBI database. It gives an indication that the species of analyzed material belongs to Panthera paurdus origin. It also fulfills the requirements of column 6 mention above under sub-heading 'Objectives of invention'.

Table 5. Reference animal belonging to family felidae selected for comparison with 'adil.flesh' to confirm the findings of BLAST analysis results of which are mentioned in Table 3 and 4, respectively. The animals listed in SN. 1-21 represent different species of family felidae. SN. 22 and 23 are primate species taken for out-group comparisons.

Table 6 Multiple sequence alignments of cytochrome b sequences (328 bp) revealed from 'adil.flesh' and reference animals listed in Table 5. The positions that have a common nucleotide in all the animal species under investigation are shown with a star (*) mark;

however, the positions that are variable in any of the animals under investigation are unmarked. The nucleotides at these positions constitute the molecular signature of an individual species, which are unique and highly specific for its species. These signatures are the molecular basis of identification of individual animal species using our primers 'mcb398' and 'mcb869'.

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Table 7 (Tables 7a, 7b, 7c and 7d). The comparison of the molecular signatures of different animal species investigated along with 'adil.flesh', the confiscated skin of unknown animal origin. This table demonstrates the variable positions (i.e. the positions which are not marked with star (*) symbol in Table 6), amongst the 328 bp fragment revealed from the animals listed in Table 5. The dot (.) mark represents the presence of the similar nucleotide as listed in lane 1 i.e. the sequence from "adil flesh' at that position. It demonstrates that the signatures of each species are unique and specific to its species. The molecular signatures of 'adil.flesh' are comparable (except for position 37 which has a transition from 'T' to 'C') to the molecular signature of 'gz1L' i.e. the known leopard 'Panthera pardus' source, indicating the identity of the source of confiscated skin 'adil.flesh' as that of a leopard 'Panthera pardus' source. The nucleotide variations (at the positions 153, 198, 223, 264, among the known leopards, (i.e. gz1L, gz2L, and gz3L, respectively)), give an idea about the geographical habitat of each animals. Various studies referring to molecular evolution of different animal species support this hypothesis⁷⁵; however, it could further be confirmed by taking the reference animals from different geographical areas and analyzing by our primers 'mcb 398' and 'mcb869'. If we could generate the database of different haplotypes (i.e. habitat specific molecular signatures) of the animal species, it would also enable our primers to reveal the geographical location of the commitment of wildlife crime.

Table 8. Percent similarity matrix calculated by pair-vise comparisons of nucleotide sequences aligned (illustrated in Table 6). The cytochrome b gene sequence of DNA isolated from confiscated material had maximum similarity (99.7% and 98.2%, with the lineages of animals 'gz2L' and 'gz3L', respectively) with the sequences obtained from known normal leopard source, indicating its identity as that of a leopard origin. The similarity matrix has been calculated using the software PHYLIP (3.5).

Table 9. Animals selected for validation of minimum P,S score for efficient amplification of cytochrome b gene of different origin by the primers 'mcb398' and 'mcb869'. P,S score of primers 'AFF' and 'AFR' for these animals are shown.

Table 10. BLAST analysis of primers 'mcb398' in nr database of NCBI. It demonstrates

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that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer Table 11. BLAST analysis of primers 'mcb869' in nr database of NCBI. It demonstrates that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer.

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Table 12. Other animal belonging to distantly related animal species, investigated to confirm the universal nature of primers 'mcb398' and 'mcb869'. Gel photograph showing the PCR amplicons from these animals are shown in Figure 4.

The mitochondrial cytochrome b gene has very widely been used in molecular taxonomic studies. It has immense capabilities to reveal different evolutionary lineages of animals in family, genus and species specific manner. It has also been used to classify the population of a particular species according to its demographic distributions⁷⁵. The vast database of cytochrome b sequences of different animal species has accumulated in public databases such as Genbank and NCBI¹⁻⁶⁵. We have explored these unique characteristics of cytochrome b gene to establish the identity of confiscated remains of any unknown animal by inventing a pair of novel primers, 'mcb398' and 'mcb869', that can amplify a small fragment (472 bp) of cytochrome b gene of wide range of animal species in universal manner. These primers work universally because its 3' ends target within a highly conserved region.

The fragment of cytochrome b gene identified had all the features mentioned in columns 1, 2 and 3 listed under sub-heading 'Objective of invention'. We identified this fragment by aligning the cytochrome b gene sequences (1140 bp) of 221 different animal species listed in Table 1. These sequences are publicly available in NCBI DNA databases. These sequences were aligned using the software CLUSTAL X (1.8). As mentioned before, the 472 bp fragment of cytochrome b gene identified by us to have the features mentioned in columns 1, 2 and 3 listed under sub-heading 'Objective of invention' includes the nucleotides between 398 to 869 in Antilope cervicapra and Felis catus; however, 399 to 870 in Homo sapiens sapiens species. Except at few positions (marked as star (*) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, revealing the identity of the biological material belonging to that of an unknown animal origin by the procedure invented by us. As for identity of this fragment we are

considering Antilope cervicapra as a representative species, and the sequence the above fragment of cytochrome b gene of Antilope cervicapra is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of Antilope cervicapra

"taccatgaggacaaatatetttttgaggagcaacagteateaceaateteettteageaateeeatacateggtacaaacetagtaga atgaatetgaggagggtteteagtagataaageaaceettaeeegatttttegeetteeaetttateeteeeatttateattgeageeett aceatagtacacetactgttteteeaegaaacaggateeaacaaceceacaggaateteateagacgcagacaaaatteeateacececeacatattaaattttaaceeteatgettetagteetatteteaceggacetgettggag acecagacaactatacaccagcaaacecacttaatacacccccacatatcaagecegaatgatactteetatttgcatacgcaateet eegateaatteetaacaaactaggagg

Table 2 presents the alignment of the above fragment of cytochrome b gene of 221 animal species. Each species in table 2 has been represented by a unique code, which is decoded in Table 1. We selected these species to represent the vast range of animal families of distant orders. Of 221 species, about 65 were the protected/endangered or rare species listed in Wildlife (Protection) Act, 1972 (Central Act NO 53 of 1972). These species are marked with symbol (*) in Table 1. The NCBI accession number refers to its registration number in NCBI database and the number in superscript represent the reference cited. Based on the aligned cytochrome b sequences of different 221 animal species the primers designed were as follow:

Primers name Sequence (5'-3')

20 'mcb398'

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"TACCATGAGGACAAATATCATTCTG"

'mcb869'

"CCTCCTAGTTTGTTAGGGATTGATCG"

Tables 2, 10 and 11, respectively, demonstrates that the 3' ends of the primers are highly conserved amongst all the animal species analyzed in-silico (In total 221 animal species listed in Table 1 and about 500 species listed in Tables 10 and 11, respectively) Also, the 5' end of the primers were selected within the conserved region of cytochrome b gene to improve the probability and stability of match of the primers to their target sequences (i.e. the above mentioned 472 bp fragment of cytochrome b gene). The primers were thoroughly checked for internal stabilities, loop or dimmer formation using different software 'Amplify (1.2)''Primer3' (http://www.genome.wi.mit.edu/cgi-<u>bin/primer/primer3.cgi</u>) as well as manually. We assigned the P,S score (P=Probability of match, S=Stability of match) to the primers for each template using the software Amplify (1.2). The higher scores of P and S ensure a good amplification if all other conditions standard (which are mentioned under 'Example 3') are optimum. The Highest score for 'mcb398' was 98,63 (i.e. the situation where the primer has perfect match with template);

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however, the highest P, S for 'mcb869' was recorded as 98, 68 for a complete match between the primer and template. The lowest P,S score observed for 'mcb398' was 81,50 for species Talpa europaea whereas 'mcb869' had a high P, S score for this species (92, 57). The another species which have lowest P, S score for one of the two primers were Eumeces egregious and Equus ainus. Eumeces egregious had P, S score 86, 55 and 73,51 for 'mcb398' and 'mcb869', respectively; however, the P, S score of Equus ainus was calculated as 91,61 and 73, 51 for 'mcb398' and 'mcb869', respectively. All other animals had higher P, S scores then the above mentioned species. To ensure that these primers would work efficiently with the DNA template from the animals having the lowest P, S score for one of the primers, we designed an another experiment to validate the lower limits of one of the two primers sufficient for efficient amplification in PCR. We designed (AFF= 5'tagtagaatgaatctgaggagg3' and another primer an pair AFR=5'atgcaaataggaagtatcattc3'.) having more mis-pairing at their annealing sites (but not at ends), therefore have less internal stability and lower P, S scores for its templates (listed in Table 9). The P,S scores of 'AFF' and 'AFR' were as calculated as low as 41 and 49 for Platanista gangetica and Sus scrofa These species were amplified efficiently using the primers 'AFF' and 'AFR' (results shown in Figure 3) (keeping all other conditions standard i.e. the conditions mentioned in 'Example 3'). The lowest P,S scores (86, 55 and 73,51 for species Eumeces egregious) for our primers 'mcb398' and 'mcb869', respectively, were higher then the above range of combined P, S scores of 'AFF' and 'AFR' for species Sus scrofa (87, 52 and 87, 41), which was efficiently amplified by the primers 'AFF' and 'AFR'. It gives an indication that the primers 'mcb 398' and 'mcb 869' would work with all the species including Eumeces egregious efficiently to give rise to the expected product in PCR. This experiment confirmed that the primers 'mcb398' and 'mcb 869' are capable of amplifying the cytochrome b fragment of most of the animal species in a universal manner.

For further confirmation of universal nature of our primers, we blasted the sequence of our primers against the *mito* and *nr* databases of NCBI using BLAST software. The results of these analyses are shown in Tables 10, and 11, respectively.

Finally, the universal nature of the primers was tested in our laboratory with some more animal species listed in Table 12. These primers amplified all the animal species efficiently, giving rise to the band of expected size (472 bp). The results are shown in Figure 4. This experiments substantiated the results of P,S analysis and other *in-silico* analyses to show that the primers 'mcb398' and 'mcb 869' are universal primers.

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The flow chart of establishing identity of the species of biological material of unknown animal origin using primers 'mcb398' and 'mcb869'

Biological material of unknown animal origin

DNA isolation

PCR amplification of DNA isolated using primers 'mcb398' and 'mcb869'

Sequencing at both the strands in triplicate (using any standard procedure of sequencing such as using ABI

Prism 3700, PE-Applied Bio-systems)

BLAST of revealed sequence in mile database of NCBI (http://www.ncbi.nlm.nih.gov/BLAST)

(it gives idea about the family of the analyzed material by producing the most significant alignment of the query sequence with the sequences registered in database)

BLAST of revealed sequence in nr database of NCBI

(http://www.ncbi.nlm.nih.gov/BLAST

(it gives idea about the Genus or more precisely, species of the analyzed material by producing the most significant alignment of the query sequence with the sequences registered in database)

Selection of reference animals belonging to the family/Genus/and species revealed by mito and nr BLAST searches

Isolation of DNA from the blood of known reference animals; PCR amplification using primers 'mcb398' and 'mcb869'; sequencing of the PCR products in triplicate using the same primers

Multiple sequence alignments of the revealed sequences of mitochondrial cytochrome b gene of known reference animals and the biological material of unknown animal origin using software such as

Autoassembler (/CLUSTAL X (1.8)

Identification of sequence from the aligned sequences

that is homologous (or significantly similar) to the cytochrome b gene sequence of the DNA obtained from biological material of unknown animal origin.

The species of homologous sequence would be the species of the biological material under investigation

Examples

Example 1

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Example for identification of a fragment of cytochrome b gene fulfilling the requirements of columns 1, 2 and 3 mentioned under sub-heading 'Objectives of invention' of heading 'Brief summary of invention'

The cytochrome b molecule has very vastly been used in molecular taxonomic studies. Being a slow evolving gene. It has a tremendous information in its nucleotide sequences to distinguish the animals to their family, genus and species sources 1-65. A vast database of the sequences of cytochrome b gene of different animal species has accumulated in the nr and mito databases of NCBI. We have explored these qualities of cytochrome b gene to establish the identity of confiscated remains of unknown animal origin to its family, genus and species sources. For this purpose, we have identified a fragment of cytochrome b gene which is highly polymorphic inter-specifically, however, it is monomorphic among the individual of same species, therefore it can group the individual of an unknown species with the known individuals of reference species to which it belongs. In order to amplify this fragment from DNA isolated form any unknown origin, it was necessary that it remain flanked with the highly conserved sequences amongst a vast range of animal families. To identify such a unique fragment within the cytochrome b gene, we aligned the sequences of 221 distantly related animal species (listed in Table 1) representing various families using software CLUSTAL X (1.8). These sequences were obtained from public database NCBI (http://www.ncbi.nlm.nih.gov). The aligned data was examined carefully for the conserved sites amongst all the species included in in-silico analysis. We identified a fragment (472 bp) of cytochrome b gene that was fulfilling all the requirements mentioned above and also under column 1, 2 and 3 of sub-heading 'Objectives of invention'.

As for the identity of this fragment we would like to mention that it includes the nucleotides between 398 to 869 in Antilope cervicapra and Felis catus; however, 399 to 870 in Homo sapiens sapiens species. Except at few positions marked as star (*) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, giving rise to their unique molecular signature. These molecular signatures are characteristic of its species and form the basis of revealing the identity of the biological material of an unknown animal origin by the procedure invented by us. Considering Antilope cervicapra as a representative species, the sequence of this fragment is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of Antilope cervicapra

"taccatgaggacaaatatctttttgaggagcaacagtcatcaccaatctcctttcagcaatcccatacatcggtacaaacctagtaga atgaatctgaggagggttctcagtagataaagcaacccttacccgatttttcgccttccactttatcctcccatttatcattgcagccctt accatagtacacctactgtttctccacgaaacaggatccaacaaccccacaggaatctcatcagacgcagacaaaattccattccac ccctactacactatcaaagatatcctaggaggctctactattaattttaaccctcatgcttctagtcctattctacacggacctgcttggag acccagacaactatacaccagcaaacccacttaatacacccccacatatcaagcccgaatgatacttcctatttgcatacgcaatcct ccgatcaattcctaacaaactaggagg"

Example 2:

Example for development of universal primers to amplify the fragment identified mentioned under 'Example 1'.

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A pair of universal primer was designed which has the following features:

- 1. It targets the fragment identified (mentioned under 'Example 1') to amplify it in polymerase chain reaction (PCR).
- 2. Its 3' and 5' ends that are highly conserved (marked as star (*) in Table 2), amongst a vast range of animal species ensuring the amplification of the fragment mentioned above in a universal manner. The sequencing of the fragment amplified by these primes reveals the molecular signature of the species of analyzed material, which on comparison with the sequences of the known reference animals reveals the identity of the species of unknown biological material under investigation.
- 3. The tm (melting temperature) of both primers was almost similar (about 58 degree centigrade) ensuring the significant annealing of both the primers to its template, therefore significant amplification of targeted region in PCR.
 - 4. The internal stability and P, S, score of the primers were ensured higher while designing it. The possibilities of internal loop formation, dimmer formation etc were also excluded by selecting its sequence uniquely. This ensured that the primer would be a good primer to be used in PCR for amplification of DNA from unknown animal origin.
 - 5. The 3' end of the primers were ensured to have either 'G' or 'C' to increase the probability of strong bonding at its 3'ends, which is necessary for efficient amplification of DNA template in PCR. It also strengthens the universal nature of the primer.
 - 6. The sequences of the primers were ensured to be unique so that it does not give rise to non-specific and spurious products in PCR leading to confusion. It improved the efficiency and quality of the technique invented by us.

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- 7. These primers were named as 'mcb398' and 'mcb869' because of its property to amplify a region of mitochondrial cytochrome b gene between nucleotides 398 to 869 of Antilope cervicapra, a representative animal species for this invention. We took this animal species as representative species because the idea of developing such a novel primers came in the mind of inventors while they were working on the genome of this animal in Centre for Cellular and Molecular Biology, Hyderabad, India.
- 8. The sequences of the universal primers invented are as follows:

Primers name

Sequence (5'-3')

10 'mcb398'

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"TACCATGAGGACAAATATCATTCTG"

'mcb869'

"CCTCCTAGTTTGTTAGGGATTGATCG"

Example 3:

Example for development of universal PCR conditions to ensure the amplification of a template of any unknown origin in PCR, hence strengthening the universal nature of the technique invented by us

The PCR conditions developed had the following unique features:

- 1 These were capable of amplifying the DNA template of any animal origin in an universal manner using the universal primers mentioned under 'Example 2'.
- 2. The conditions were selected to ensure the comparable annealing temperature for both the primers i.e. 'mcb398' and 'mcb869'.
- 3. The PCR conditions standardized herewith are universal; therefore, the possibility of PCR failure with a template of unknown origin due to non-standard conditions is excluded. It ensures the universal nature of our technique to be used in wildlife forensics.
- 4. The universal conditions mentioned above are:

Amplification reactions should be carried out in 20 µl reaction volume containing approximately 20 ng of template DNA, 100µm each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl₂, 0.5 unit of AmpliTaq Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed should be: an initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step at 35th cycles should be held for 10 min.

Example 4:

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Establishing the universal nature of our primer and experimental evidences to demonstrate the universal nature of primers:

The universal nature of the primers 'mcb398' and 'mcb 869' was ensured by the following measures:

(a) Selecting the primers from the aligned cytochrome b gene sequences of 221 animal of distantly related species:

The cytochrome b gene sequences (1140 bp) were aligned using software CLUSTAL X (1.8). The region of cytochrome b gene that was most conserved amongst 221 animal species was selected to design the primers.

(b) Selecting the 3' and 5' ends of the primers at the highly conserved positions of cytochrome b gene:

The 3' and 5' ends of the primers were ensured to anneal to a highly conserved position amongst 221 animal species representing a vast range of animal families. It was done to ensure an efficient amplification of all the species in PCR. These positions are shown with star (*) mark in Table 2.

(c) Ensuring either 'G' or 'C' at the 3' end of the primers:

It was ensured the primers to have either 'G' or 'C' at its 3' ends as these are the nucleotides that ensure the strong bonding at the 3' ends of the primers due to three hydrogen bonds while pairing with each other. The strong bonding at 3' ends nelps the primers to anneal properly with its template resulting in significant amplification in PCR.

(d) Selecting the sequences of the primers to ensure a higher internal stability, higher P, S score, and no primer dimmer and loop formation:

The sequences of the primers were selected to have a high P, S score for a vast range of animal species (Shown in Table 1). The care was taken to exclude the possibilities of loop or primer dimmer formation that could reduce the efficiency of the primers in PCR.

(e) Selecting the sequence of the primers with a comparable melting temperature:

The sequences of the primers were selected to have a comparable melting temperature so that these could work together to amplify a DNA template in PCR at a similar annealing temperature. The melting temperature of both the primers was about 58 degree centigrade and the annealing temperature used in PCR is 51 degree centigrade.

Experimental evidences to demonstrate the universal nature of primers:

(1) Evidence from In-silico analysis:

(a) Selecting the primers within the most conserved region of mitochondrial cytochrome b

As mentioned above, the primers were designed to anneal within a highly conserved region of mitochondrial cytochrome b gene fragment of 472 bp. Table 2 presents the alignment of the above fragment of cytochrome b gene of 221 animal species representing a vast range of animal families. The conserved positions of nucleotide sequences are shown with star (*) mark in Table 2

Table 2 also demonstrates that the 3' ends of the primers are highly conserved amongst all the animal species analyzed *in-silico*. In the aligned sequences, the conserved nucleotides are marked with symbol (*). Also, the 5' end of the primers were selected within the conserved region of cytochrome b gene to improve the probability and stability of match of the primers to their target sequences (i.e. the above mentioned 472 bp fragment of cytochrome b gene). The primers were thoroughly checked for internal stabilities, loop or dimmer formation using different software viz., 'Amplify (1.2)', 'Primer3' (http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi) as well as manually.

(b) P, S, score analysis:

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We assigned the P,S score (P=Probability of match, S=Stability of match) to the primers for each template using the software Amplify (1.2). The higher scores of P and S ensure a good amplification if all other conditions standard (which are mentioned under 'Example 3') are optimum. The Highest score for 'mcb398' was 98,63 (i.e. the situation where the primer has perfect match with template); however, the highest P, S for 'mcb869' was recorded as 98, 68 for a complete match between the primer and template. The lowest P,S score observed for 'mcb398' was 81,50 for species Talpa europaea whereas 'mcb869' had a high P, S score for this species (92, 57). The another species which have lowest P, S score for one of the two primers were Eumeces egregious and Equus ainus. Eumeces egregious had P, S score 86, 55 and 73,51 for 'mcb398' and 'mcb869', respectively; however, the P, S score of Equus ainus was calculated as 91,61 and 73, 51 for 'mcb398' and 'mcb869', respectively. All other animals had higher P, S scores then the above mentioned species. To ensure that these primers would work efficiently with the DNA template from the animals having the lowest P, S score for one of the primers, we designed an another experiment to validate the lower limits of one of the two primers sufficient for efficient amplification in PCR. We designed an another (AFF= 5'ctagtagaatgaatctgaggagg^F and AFR= 5'tatgcaaataggaagtatcattc^F.) that have more mis-pairing at their annealing sites (but not at ends), therefore have less internal stability

and lower P, S scores for its templates (listed in Table 9). The P,S scores of 'AFF' and 'AFR' were as calculated as low as 41 and 49 for *Platanista gangetica* and *Sus scrofa* These species were amplified efficiently using the primers 'AFF' and 'AFR' (results shown in Figure 3) (keeping all other conditions standard i.e. the conditions mentioned in 'Example 3'). The lowest P,S scores (86, 55 and 73,51 for species *Eumeces egregious*) for our primers 'mcb398' and 'mcb869', respectively, were higher then the above range of combined P, S scores of 'AFF' and 'AFR' for species *Sus scrofa* (87, 52 and 87, 41), which was efficiently amplified by the primers 'AFF' and 'AFR'. It gives an indication that the primers 'mcb 398' and 'mcb 869' would work with all the species including *Eumeces egregious* efficiently to give rise to the expected product in PCR. This experiment confirmed that the primers 'mcb398' and 'mcb 869' are capable of amplifying the cytochrome b fragment of most of the animal species in a universal manner.

© BLAST analysis:

The sequences of primers 'mcb398' and 'mcb869' were blasted against mito and nr databases of NCBI to see its significant alignments with the sequences registered in GenBank. As expected, the most significant alignments of the sequences were found with the cytochrome b gene regions (within the 472 bp fragment mentioned in 'Example 1') of different animal species. This analysis also showed that the 3' as well as 5' ends of the primers were highly conserved amongst a vast range of animal species, confirming the universal nature of the primers (Tables 10 and 11, respectively)

(2) Evidence from bench work/experiments done in laboratory conditions:

The DNA from different animals belonging to distantly related species (mentioned in Table 12) was isolated and subjected to PCR amplification using the primers invented by us i.e. the primers 'mcb398' and 'mcb869' The PCR products amplified were resolved in agarose gel by electrophoresis and visualized under UV light. The PCR products of expected size (472bp) were obtained from all the animals confirming the universal nature of our primers. These results are shown in Figure 4.

Example 5:

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Example to establish the identity of confiscated remains from unknown animal original using the universal primers 'mcb398' and 'mcb869'.

The step-vise procedure to establish the identity of the biological material from an unknown animal source is mentioned below:

Biological material of unknown animal origin

DNA isolation

PCR amplification of DNA isolated using primers 'mcb398' and 'mcb869'

Sequencing at both the strands in triplicate (using any standard procedure of sequencing such as using ABI Prism 3700, PE-Applied Bio-systems)

BLAST of revealed sequence in mito database of NCBI

(http://www.ncbi.nlm.nih.gov/BLAST

(it gives idea about the family of the analyzed material by producing the most significant alignment of the query sequence with the sequences registered in database)

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BLAST of revealed sequence in nr database of NCBI

(http://www.ncbi.nlm.nih.gov/BLAST

(it gives idea about the Genus or more precisely, species of the analyzed material by producing the most significant alignment of the query sequence with the sequences registered in database)

Selection of reference animals belonging to the family/Genus/and species revealed by mito and nr BLAST searches

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Isolation of DNA from the blood of known reference animals;

PCR amplification using primers 'mcb398' and 'mcb869'; sequencing of the PCR products in triplicate using the same primers

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Multiple sequence alignments of the revealed sequences of mitochondrial cytochrome b gene of known reference animals and the biological material of unknown animal origin using software such as Autoassembler/CLUSTAL X (1.8)

Identification of sequence from the aligned sequences

that is homologous (or significantly similar) to the cytochrome b gene sequence of the

DNA obtained from biological material of

unknown animal origin.



The species of homologous sequence would be the species of the biological material under investigation



Application of the above information for the objectives mentioned in columns 7-13 under sub-heading 'Objective of invention' of heading 'Summary of invention'

Example 6:

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The actual execution of the technique invented

As a first application and to demonstrate the ease and utility of this method, we investigated a case of forensic identification submitted at our laboratory to seek scientific opinion on animal hunting evidence. In this case, we received the half burned remains of an unknown animal, confiscated by the crime investigation agencies. The DNA was isolated from the above material following standard methods⁷⁴ and subjected to PCR amplification using the primers mentioned above (viz., 'mcb398' and 'mcb869'). Amplification reactions were carried out in 20 µl reaction volume containing 20 ηg of template DNA, 100µm each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl₂, 0.5 unit of AmpliTaq Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed were: an initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step at 35th cycles was held for 10 min.

The PCR products obtained were sequenced in automated work station (ABI Prism 3700, PE-Biosystems) on both strands in triplicate and the sequence resolved (328 bp, shown in Figure 1a) was blasted against *mito* databases of NCBI using BLAST program⁷³. The most significant alignment (bits Value 365, E value e⁻¹⁰¹) of this sequence was produced with the cytochrome b gene sequence of *Felis catus*, (Table 3) indicating that species of

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analyzed material belongs to family felidae. Further, the above sequence revealed from the confiscated remain was blasted against nr databases of NCBI using BLAST program. The most significant alignment (bits Value 603, E value e⁻¹⁷⁰) of this sequence was produced with the cytochrome b gene sequence of Panthera pardus (Table 4), indicating the identity of the analyzed material as that of a Panthera pardus source. Based on this information, we selected the reference animals listed in Table 5 representing different species and subspecies of felidae. The DNA isolated from reference animals was amplified and sequenced on both strands in triplicate using the primer pair mentioned above. Consensus sequences obtained were aligned using program CLUSTAL X (1.8) (Table 6). Sequence comparisons identified 113 variable sites in total amongst all animals analyzed (Table 7). Pair-vise comparisons of sequences were performed to find out the variation among different animals investigated. All the species investigated were differentiated by a their unique nucleotides sequences. The molecular signatures of different reference animals were compared with the molecular signature of the confiscated skin 'adil.flesh'. Table 7 demonstrate that the maximum similarity of the adil.flesh with 'gzll' i.e. known Leopard (Panthera pardus) species, indicating the identity of the adil flesh, the confiscated skin, as that of a Panthera pardus origin. We also calculated the similarity matrix showing the pairvise similarity amongst the animal species under investigation using PHYLIP software This matrix is shown in Table 8. It demonstrates that the animals belonging to different species had more variation; however, the animals of same species had maximum similarity among their cytochrome b sequences. The cytochrome b gene sequence of DNA isolated from confiscated material had maximum similarity with the sequences obtained from known Leopard source(99.7%, and 98.2 with 'gz11' and 'gz21', respectively); establishing the identity of the source of confiscated material as that of a Normal leopard (Penthera pardus) species. The step-vise procedure involved in above analysis is illustrated in Figure la, lb and lc, respectively.

Thus, the primers invented by us can generate the molecular signature from any biological material of unknown animal origin, which actually is the characteristic of its family, genus and more precisely, the species. When these signatures are compared *in-silico* with the signatures already available in public databases (viz., GenBank, NCBI database etc) using *BLAST* software⁷³, it indicates identity of the family, genus or species of the analyzed material, which in turn is confirmed practically by comparing with the reference animals of the revealed family, genus or species, by including them in the further analysis by the primers 'mcb398' and 'mcb869'. Application of the information revealed could be in

fulfilling the requirements of objectives mentioned in columns 7-13 under sub-heading 'Objective of invention' of heading 'Summary of invention'

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The method of the invention can be used to establish the identity of confiscated animal parts and products is one of the key requirements of wildlife identification in forensics. It is needed to establish the crime with the criminal beyond a reasonable doubt to avoid the human violation of wildlife resources. Various morphological biochemical and molecular approaches have been given for this purpose; however, none of the current methods is universally applicable to detect the mutilated animal remains of unknown origin. We have identified a fragment on the mitochondrial cytochrome b gene, which has enormous information to differentiate among various animal species back to the family, genus and species sources. We have also found that this fragment is flanked by the highly conserved sequences amongst a vast range of animal species. We invented a pair of universal primer that can amplify this fragment of DNA isolated from the biological material of an unknown animal origin in polymerase chain reaction (PCR) to reveal its identity at species and sub-species sources. This novel invention has great potential to revolutionize the whole scenario of wildlife forensic identification and crime investigation.

Table 1. The animal species included in the study for in-silico analysis

SN.	Code	Name	NCBI accession #	°P,S/F	*P,S/R
1	aep.mel	Aepyceros melampus	AF0362891	97,60	94, 62
2	ore.ore	Oreotragus oreotragus	AF0362881	88, 52	94, 62
3	add.nas	Addax nasomaculatus	AF034722 ²	97, 60	95, 66
4	ory.dam	Oryx damah	AJ2226851	90, 58	95, 66
5	hip.equ	Hippotragus equinus	AF022060 ³	98, 63	85,55
6	alc.bus	Alcelaphus buselaphus	AJ2226811	97,60	98, 68
7	sig.lic	Sigmoceros lichtensteinii	AF0349674	97,60	98, 68
8	bea.hun	Beatragus hunteri	AF0349684	97,60	94, 62
9	dam.lun	Damaliscus lunatus	AF0166353	97, 60	77,55
10	con.tau	Connochaetes taurinus	AF0166383	82, 56	93, 62
11	bis.bon	Bison bonasus	Y150055	90, 58	87, 63
		Bos grunniens*	AF0916316	90, 58	94, 62
12	bos.gru bos.tra	Bos tragocamelus*	AJ2226791	90, 58	95, 66
13		Bubalus bubalis*	D34637 ⁷	97, 60	93, 64
	buba.bub	Bubalus mindorensis	D82895 ⁸	97, 60	87,62
	bub.min	Tragelaphus angasii	AF0916336	97, 60	87, 63
	tra.ang	Tragelaphus eurycerus	AF0362761	90, 58	97, 64
17 18	traleur	Nemorhaedus caudatus*	U17861°	95, 6l	93, 59
	nem.cau	Pseudois nayaur	AF034732 ²	89, 55	89, 59
19 20	pse.nay amm.ler	Ammotragus lervia	AF034731 ²	94, 58	97, 63
21	cap.fal	Capra falconeri*	D8420210	98, 63	95, 66
22	cap.ibe	Capra ibex*	AF0347352	98, 63	89, 58
23	hem.jem	Hemitragus jemlahicus*	AF034733 ²	95, 61	90, 61
24	гир.руг	Rupicapra pyrenaica	AF034726 ²	95, 61	89, 59
25	rup.rup	Rupicapra rupicapra	AF034725 ²	95, 61	94, 64
	pan.hod	Pantholops hodgsoni	AF034724 ²	98, 63	95, 66
27	•	Budorcas taxicolor taxicolor*	U17868°	90, 53	95, 66
	ovi.amm	Ovis ammon*	AF034727 ²	98, 63	97, 64
29	ovi.vig	Ovis vignei •	AF034729 ²	98, 63	97,64
30	cap.cri	Capcornis crispus *	AJ304502 ¹¹	98, 63	94, 63
. 31	ovi.mos	Ovibos moschatus	U17862°	98, 63	92, 61
32	ore.ame	Oreamnos americanus	AF19063212	98, 63	94, 62
33	c cp .dor	Cephalophus dorsalis	AF0916346	97, 58	90, 61
34	cep.max	Cephalophus maxwellii	AF096629 ¹³	97, 60	88, 53 93, 59
35	alc.alc	Alces alces	AJ000026 ¹⁴	95, 61	90, 63
36	hyd.ine	Hydropotes inermis	AJ00002814	97, 60 90, 58	93, 64
37	mun.mun	Muntiacus muntjak*	AF04271815	98, 63	82, 59
38	cer.ele.kan	Cervus elaphus kansuensis*	AB02109816	98, 63	82.59
39	cer.ele.xan	Cervus elaphus xanthopygus	AB021097 ¹⁶ AB021096 ¹⁶	98, 63	90.61
40	cer.ele.can	Cervus elaphus canadensis*	AB0210941*	98, 63	90.61
41	cer.nip.ce	Cervus nippon centralis Cervus nippon yesoensis	AB0210951*	98, 63	90, 61
42 43	cer.nip.ye cer.nip.ke	Cervus nippon keramae	AB02109114	93, 63	90, 61
4.)	cer.mp.ke	Cervus nippon serumae	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		

			16	09 67	00.61
44	cer.nip.pu	Cervus nippon pulchellus	AB021090 ¹⁶	98, 63	90, 61
45	cer.nip.ni	Cervus nippon nippon	AB021093 16	98, 63	90, 61
46	cer.ela.sc	Cervus elaphus scoticus	AB02109916	98, 63	90, 61
47	cer.dam	Cervus dama	AJ00002214	98, 63	88, 53
43	ran.tar	Rangifer tarandus	AJ00002914	98, 63	89, 57
49	mos.fus	Moschus fuscus *	AF026333'7	90, 59	90, 61
50	mos.leu	Moschus leucogaster*	AF026889'7	90, 59	90, 61
51	mos.chr	Moschus chrysogaster*	AF026887 ¹⁷	90, 59	90, 61
52	mos.ber	Moschus berezovskii*	AF026886 ¹⁷	90, 59	90, 61
53	mos.mos	Moschus moschiferus*	AF026883 ¹⁷	90, 59	92, 61
54	kob.ell	Kobus ellipsiprymnus	AF022059 ³	91,61	95, 66
55	kob.meg	Kobus megaceros	AJ2226861	91,61	83, 56
56	red.aru	Redunca arundinum	AF096623 ¹³	91,61	94, 62
57	red.ful	Redunca fulvorufula	AF036284 ^t	89, 57	94, 62
58	neo.mos	Neotragus moschatus	AJ2226831	89, <i>5</i> 7	94, 62
59	pel.cap	Pelea capreolus	AF022055 ³	91,61	90, 61
60	anticer	Antilope cervicapra *	AF022058 ³	82, 56	93, 64
61	sai.tat	Saiga tatarica	AF06448718	91,61	92, 61
62	gaz.dam	Gazella dama	AF0259543	91,61	92, 61
63	our.our	Ourebia ourebi	AF036288 ¹	82, 56	82, 59
64	gaz.gaz	Gazela gazella*	AJ2226821	91,61	89, 57
65	rap.mel	Raphicerus melanotis	AF0220533	81,54	80, 50
66	mad.kir	Madoqua kirkii	AF022070 ³	90, 58	97, 65
67	antame	Antilocapra americana	AF0916296	98, 63	98, 68
68	tra.jav	Tragulus javanicus*	D32189 ¹⁹	86, 57	86, 59
69	рагизр	Tragulus napu*	X56288 ²⁰	81, 52	93, 58
70	bal.acu	Balaenoptera acutorostrata	X75753 ²¹	89, 56	97, 61
71	bal.bon	Balaenoptera bonaerensis	X75581 ²¹	89, 56	93, 59
72	bal.bor	Balaenoptera borealis*	X75582 ²¹	89, 56	93, 59
73	bal.edi	Balaenoptera edeni	X75583 ²¹	89, 56	83, 54 86, 57
74	esc.rob	Eschrichtius robustus	X75585 ²¹	97, 61 97, 57	93, 59
75	bal.mus	Balaenoptera musculus •	NC_001601 ²²	97, 57 97, 61	94, 63
76	meg.nov	Megaptera novaeangliae •	X75584 ²¹	97, 57	94, 63
77	bal.phy	Balaenoptera physalus*	NC_001321 ²³	93.55	91,53
78	cap.mar	Caperea marginata	X75586 ²¹ AF084073 ²⁴	85, 51	33,55
79	cep.com	Cephalorhynchus commersonii	AF084072 ²⁴	85, 51	92, 59
80	cep.eut	Cephalorhynchus eutropia*	AF084072 AF084067 ²⁴	94, 59	92, 59
81 82	lag.obl cep.hea	Lagenorhynchus obliquidens Cephalorhynchus heavisidii	AF084070 ²⁴	89, 56	97, 63
	cep.hec	cephalorhynchus hectori*	AF08407124	89, 56	92, 59
84	lag.aus	Lagenorhynchus australis	AF08406924	86. 54	92. 59
	lag.cru	Lagenorhynchus cruciger	AF08406824	86.54	92.59
	lag.obs	Lagenorhynchus obscurus	AF08406614	86. 54	92, 59
	lis.bor	Lissodelphis borealis	AF08406424	85.51	92. 59
	lis.per	Lissodelphis peronii	AF084065**	86. 54	92, 59
	glo.mac	Globicephala macrorhynchus	AF08405524	94, 59	88, 55
90	glo.mel	Globicephala melas	AF084056 ¹⁴	94, 59	\$8. \$5
91	fer.att	Feresa attenuata*	AF08405224	94, 59	92, 59

		AF084053 ²⁴	94, 59	88, 55
92 pep.elc	Peponocephala electra*	AF084059 ²⁴	97,61	89, 59
93 gra.gri	Grampus griscus	AF084057 ²⁴	94, 59	92, 59
94 pse.cra	Pseudorca crassidens*	AF0840775 ²⁴	98, 63	89.59
95 lag.acu	Lagenorhynchus acutus	AF084061 ²⁴	86, 57	82, 52
96 arci.bre	Orcinus orca		86, 57	91,54
97 orca.bre	Orcaella brevirostris	AF084063 ²⁴	96, 54	97,63
98 del.cap	Delphinus capensis	AF084087 ²⁴		97, 63
99 del.tro	Delphinus tropicalis	AF08408S ²⁴	97, 57	-
100 del.del	Delphinus delphis	AF08408524	97, 57	97, 63
101 sten.cly	Stenella clymene	AF084083 ²⁴	97, 57	97,63
102 sten.coe	Stenella coeruleoalba	AF084082 ²⁴	97, 57	97, 66
103 tur.adu	Tursiops aduncus	AF084092 ²⁴	97, 57	97, 63
104 sten.fro	Stenella frontalis	AF084090 ²⁴	97, 57	97, 63
105 saus.chi	Sousa chinensis	AF084080 ²⁴	97, 57	88, 59
106 sten.lon	Stenella longirostris	AF084103 ²⁴	97,61	97, 63
107 turs.tru	Tursiops truncatus	AF084095 ²⁴	97, 57	96, 59
108 lage.alb	Lagenorhynchus alborostris	AF084074 ²⁴	97,61	97,66
109 sten.bre	Steno bredanensis	AF084077 ²⁴	97, 61	94, 64
110 sota flu	Sotalia fluviatilis	AF304067 ²⁵	97,61	97,63
111 del.leu	Delphinapterus leucas	U72037 ²⁶	97, 61	95, 66
112 mono.mon	Monodon monoceros	U72038 ²⁶	97, 61	95,66
113 plat.gan	Platanista gangetica*	AF304070 ²⁵	97, 61	86, 59
114 plat.min	Platanista minor*	X92543 ²⁷	97, 61	86, 59
115 kogi.bre	Kogia breviceps	U72040 ²⁶	97, 59	90, 63
116 kogi.sim	Kogia simus	AF304072 ²⁸	96, 55	92, 63
117 phys.cat	Physeter catodon	AF304073 ²⁵	97, 57	80, 58
118 lipo.vex	Lipotes vexillifer*	AF30407125	89, 56	83, 53
119 phoc.sin	phocoena sinus	AF08405124	87, 49	92, 62
120 bera bai	Berardius bairdii	X92541 ²⁷	96, 55	90, 59
121 ziph.car	Ziphius cavirostris	X92540 ²⁷	97,61	89,57
122 meso.eur	Mesoplodon europaeus	X92537 ²⁷	97, 57	90, 61
123 meso.bid	Mesoplodon bidens	X92538 ²⁷	97,61	92, 61 94, 63
124 meso.den	Mesoplodon densirostris	X92536 ²⁷	91,61	90,65
125 hype.amp	Hyperoodon ampullatus*	X92539 ²⁷	97, 61	36, 58
126 meso.per	Mesoplodon peruvianus	AF304074 ²⁵	97,61	88, 55
127 pont.bla	Pontoporia blainvillei	AF304069 ²⁵	92, 59	95.66
128 hipp.amp	Hippopotamus amphibius	Y0881329	92, 58 98, 63	97, 66
129 hex.lib	Hexaprotodon liberiensis	Y0881429	90, 59	87, 61
130 chin.son	Rhinoceros sondaicus *	AJ245725 ¹⁰	90, 59	90, 63
131 cera	Ceratotherium simum	NC_00130512	90, 59	86. 57
132 dic.sum	Dicerorhinus sumatrensis	AJ245723 ³⁰	91,61	73.51
133 equu	Equus asinus	NC_001788 ³⁴ Z50106 ³³	39, 56	85.56
134 baby.bab	Babyrousa babyrussa	Z20090 ₁₁	90, 59	87, 54
135 phac.afr	Phacochocrus africanus	250090 AF136549 ¹⁴	97. 57	83.54
136 sus.scr.ew	Sus scrofa haplotype EWB3*	Z50107 ¹¹	97. 57	85.55
137 sus.bar	Sus barbatus	U06429 ¹¹	89.55	85. 53
138 lama.gla	Lama glama	Y088125"	83, 54	86. 57
t 19 Tama.gua	lama guanicae	1.000.00		

			U06430 ³³	89, 55	85, 53
140	vic.vic	Vicugna vicugna	U06427 ³³	94, 58	86, 58
141	cam.bac	Camelus bactrianus	X\$2293 ³⁶	97, 60	87, 64
142	arc.for	Arctocephalus forsteri	X32292 ³⁶	94, 58	87,64
143	arc.gaz	Arctocephalus gazella		97, 57	86, 57
144	eum.jub	Eumetopias jubatus	X32311 ³⁶	89, 55	86, 57
145	zal.cal	Zalophus californianus	X\$2310 ³⁶	91.61	81,52
146	odo.ros	Odobenus rosmarus	X32299 ³⁶	90, 58	87, 64
147	pho.vit	Phoca vitulina	X32306 ¹⁶	98, 63	95, 66
148	pho.fascia	Phoca fasciata	X82302 ³⁶	92, 59	90, 61
149	pho.gro	Phoca groenlandica	X82303 ³⁶	89, 56	87, 64
	cys.cri	Cystophora cristata	X32294 ³⁶		82, 54
	hyd.lep	Hydrurga leptonyx	X32297 ³⁶	89, 55	91, 66
	lep.wed	Leptonychotes weddelli	X72005 ³⁷	98, 63	82, 59
	mir.leo	Mirounga leonina	X82298 ³⁶	89, 55	87, 63
	eri.bar	Erignathus barbatus	X32295 ³⁶	89, 56	87, 60
	mon.sch	Monachus schauinslandi	X72209 ³⁷	91,61	90, 63
	hela mal	Helarctos malayanus =	U18899 ³⁸	84, 54	
	sel.thi	Selenarctos thibetanus*	AB02091039	89, 57	87, 64
	ail.ful	Ailurus fulgen *s	X94919 ⁴⁰	93, 55	87, 64
159		Felis catus	NC_0017004	85, 56	90, 63
	can	Canis familiaris	NC_00200842	98, 58	84, 54
161		Talpa europaea	NC_002391 ⁴³	81,50	92, 57
	gla.sab	Glaucomys sabrinus	AF011738**	90, 59	82, 54 87, 60
	gla.vol	Glaucomys volans	AB03026145	90, 59	81,50
	hyl.pha	Hylopetes phayrei*	AB03025945	91,61	81,50
	petset	Petinomys setosus*	AB03026045	91,61	87, 64
	bel.pea	Belomys pearsonii*	AB03026245	91,61	90, 63
	pte.mom	Pteromys momonga *	- AB03026345	97,61	87, 64
	gala.demi	Galagoides demidojj	AF27141146	97, 58	87, 63
	pero.pot	Perodicticus potto	AF27141346	97,60 97,60	90, 61
	gala.mat	Galago matschiei	AF271409 ⁴⁶	97, 60	95, 66
	gala.moh	Galago moholi	AF271410 ⁴⁶	92, 58	87, 60
172	oto.gar	Otolemur garnettii	AF27141246	97, 60	93, 59
173	lor.tar	Loris tardigradus*	U53581 ⁴⁷	97, 60	95, 66
174	nyc.cou	Nycticebus coucang*	US3580 ⁴⁷	97, 60	86, 59
	mus	Mus musculus	NC_00156948	89, 57	80, 58
176	gon	Gorilla gorilla	NC_001645*° NC_001807*°	96, 55	84, 64
	homo	Homo sapiens sapiens	U07564 ⁵¹	97, 60	89, 59
	dug.dug	Dugong dugong*	AB002412 ⁵²	97, 60	76,57
	ele.max	Elephas maximus*	AF013760"	97,58	87, 63
	afr.con	Afropavo congensis	AF013763'	97,57	87.63
	pavo.mut	Pava muticus*	AF20072254	89.55	35, 57
	tra.bly	Tragopan blythii*	AF22983754	39.55	86, 61
	tra.sat	Tragopan saiyra* Tragopan caboti	AF20072314	39, 55	\$6,61
	tra.cob	Ггадоран синтінски *	AF028802"	89.55	81.56
	tra.tem arg.arg	Argusianus argus	AF013761"	89, 55	\$7,63
	cat.wal	Catrous wallichi*	AF02879211	88. 24	85.57
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	•	a a a a a a a a a a a a a a a a a a a	AF02879453	89.55	85, 57
	cro.cro	Crossoptilon crossoptilon*	AF028801 ⁵³	89.55	85, 57
	sym.ree	Syrmaticus reevesi*	AF028790 ⁵³	80. 48	94, 64
190	bam.tho	Bambusicola thoracica*	AF028790	97. 58	86, 61
191	fra.fra	Francolinus francolinus	AF01376253	98.63	85, 57
192	ith.cru	Ithaginis cruentus*	AF06819353	85, 56	82, 58
193	ant.par	Anthropoides paradisea	U27557 ⁵⁶		82, 52
194	ant.vir	Anthropoides virgo	U27545 ⁵⁶	84, 54	
195	gru.ant.an	Grus antigone antigone	U11060 ⁵⁷	90.53	87, 63
	gru.ant.gi	Grus antigone gillae	U11064 ⁵⁷	90, 53	87, 63
	gru.any.sh	Grus antigone sharpei	U11061 ⁵⁷	90, 58	87, 63
	gru.leu	Grus leucogeranus*	U27549 ⁵⁶	90, 53	87, 63
	gru.can.pr	Grus canadensis pratensis	U27553 ⁵⁶	97, 60	87, 63
	gru.can.ro	Grus canadensis rowani	U27552 ⁵⁶	97,60	87, 63
	gru.can.ta	Grus canadensis tabida	U2755156	98, 63	87, 63
	gru.can.ca	Grus canadensis canadensis	U27554 ⁵⁶	97,61	87, 63
	gru.ame	Grus americana	U27555 ⁵⁶	90,58	87, 63
	gru.gru	Grus grus	U27546 ⁵⁶	89, 54	87, 63
	gru.mon	Grus monacha*	U27548 ⁵⁶	90, 53	87, 63
	gru.nig	Grus nigricollis*	U2754756	90, 58	87, 63
	gru.jap	Grus japonensis	U27550 ⁵⁶	81,54	87, 63
	cic.boy	Ciconia boyciana*	NC_002196 ⁵⁸	94, 58	79, 60
	rhe.ame	Rhea americana	AF09033959	93, 63	79, 60
	antalb	Anthracoceros albirostris*	U89190 ⁶⁰	97,61	86, 59
	fal.fam	Falco femoralis	U83310 ⁶¹	97,61	86, 60
	fal.ver	Falco verpertinus	U83311 ⁶¹	97,61	85, 57
	fal.par	Falco peregrinus*	U83307 ⁶¹	97,61	84, 52
	fal.spa	Falco sparverius	U83306 ⁶¹	92, 59	80, 51
	aytame	Aythya americana	NC_000877 ⁶²	98, 63	94, 62
	smi.sha	Smithornis sharpei	NC_000879 ⁵⁹	97, 58	90, 61
	vid.cha	Vidua chalybeata	NC_000880ss	97, 60	87, 64
	chry.pic	Chrysemys picta	NC_002073 ⁶³	39, 56	86, 57
	emy.orb.ku	Emys orbicularis	AJ131425 ⁶⁴	90, 59	94, 63
	che.mud	Chelonia mydas *	AB01210465	90, 58	94, 63
	eum.egr	Eumeces egregius	AB01660655	86, 55	73, 51

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Table 2. Multiple sequence alignment of 472 bp fregment of mitochondrial cytochrome b gene of 221 animal species

PRIMER 'mcb393'	TACCATGAGGACAAATATCATTCTG	
	* ** ** ** ** ** ** ** ** * * * * * *	
aep.mel	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACAAATCTCCTCTCAGCAA 60	
019.019		
add.nas		
ory.dam	magazina ana marana mana mana mana mana mana m	
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amm.ler	THE TOTAL TO	
pse.nay		
cap.ibe		
hem.jem	TACCATGAGGACAGATATCATTCTGAGGGGCAACAGTCATCACCAATCTCCTCTCAGCAA 60 TACCATGAGGACAAATATCATTCTGAGGGGCAACAGTCATCACCAATCTCTCTC	
cap.fal	TACCATGAGGACAGATATCATTCTGAGGAGCAACAGTTATTACCAATCTCCTCTCAGCAA 60 TACCATGAGGACAGATATCATTCTGAGGAGCAACAGTTATTACCAATCTCTCTC	
rup.pyr	TACCATGAGGACAGATATCATTCTGGGGAGCAACAGTTATTACCAACCTCCTCTCAGCGA 60 TACCATGAGGACAGATATCATTCTGGGGAGCAACAGTTATTACCAACCTCCTCTCAGCA 60	
rup.rup	TACCATGAGGACAGATATCATTCTGAGGGGCAACAGTTATTACCAATCTTCTCTCAGCAA 60 TACCATGAGGACAGATATCATTCTGAGGGGCAACAGTTATTACCAATCTTCTCTCAGCAA 60	
nem.cau	TACCATGAGGACAGATATCATTCIGAGGGGCAACAGTTATTACCAACCTCCTCTCAGCAA 60 TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTCATTTACCAACCTCCTCTCAGCAA 60	
bud.tax.tax	TACCATGAGGACAAATATCATTIGAGGACAACAGTATTACCAACCTCCTTTCAGCAA 60	
pan.hod	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTAATTACCAACGTCCTTTCAGCAA 60 TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTAATTACCAACGTCCTTTCAGCAA 60	
ovi.amm	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCCTTTCAGCAA 60 TACCATGAGGACAAATATCATTCTGAGGAGGACACAGTTATTACCAACCTCCTTTCAGCAA 60	
ovi.vig	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCCTTTCAGCAA 60 ,TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCATCTCTCTC	
cap.cri	TACCATGAGGACAAATATCATTCTGAGGGGCTACAGTCATTACTAACCTCCTCTCAGCAA 60 TACCATGAGGACAAATATCATTCTGAGGGGCTACAGTCATTACTAACCTCCTCTCAGCAA 60	
evi.mos	TACCATGAGGACAAAAA CATACATTCTGAGGAGCTACAGTCATCACTAACCTCCTCTCAGCAA 60 TACCATGAGGACAAATATCATTCTGAGGAGCTACAGTCATCACTAACCTCCTCTCAGCAA 50	
ore.ame	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTIACCAATCTCCTTTCAGCAA 60 TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTIACCAATCTCTCTCAGCAA 60	
cep.dor	TACCATGAGGACAAAAAAACATCTGAGGAGGCACAGTCATTACCAACCTCCTCTCAGCAA 60 TCCCATGAGGGCAAATATCATTCTGAGGAGCCACAGTCATTACCAACCTCCTCTCAGCAA 60	
cep.max	TCCCATGAGGGCAAAAAATCATTCTGAGGAGCCACAGTCATTACCAACCTCCTCTCAGCAA 60 TCCCATGAGGACAAAAATCATTCTGAGGAGCCACAGTCATTACCAACCTCCTCTCAGCAA 60	
bis.bon	TCCCATGAGGACAAAAAATCATTTTGAGGAGCAACAGTCATTACCAACCTCCTATCAGCAA 60 TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTCATTACCAACCTCCTATCAGCAA 60	
bos.gru	TACCATGAGGACAAATATCATTTTGAGGGGCAACAGTCATTACCAACCTCCTATCAGCAA 60 TACCATGAGGACAAATATCATTTTGAGGGGCAACAGTCATTACCACCTATTATCAGCAA 60	
bos.tra	TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTTATTACCAATGTATTATCAGGAA 60 TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTTATTACCAATGTATTATCAGCAA 60	
bub.min	TACCATGAGGACAAALALCALIIIOAGGAGCAACAGTCATCACCAACCTTCTCTCAGCAA 60 TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCAACACTTCTTCTCAGCAA 60	
buba.bub	TGCATGAGGACAAAAA CATTCTGAGGGGCAACAGTCATCAGCAACCTTCTCTCAGCAA 60 TGCCATGAGGACAAAAATATCATTCTGAGGGGCAACAGTCATCAGCAACCTTCTCTCAGCAA 60	
tra.ang	TGCCATGAGGACAATATCATTCTGAGGAGGACACTGTCATCACAAACCTCCTATCAGCAA 60 TGCCATGAGGACAATATCATTCTGAGGAGGACGACTCATCACAAACCTCCTATCAGCAA 60	
tra.eur	TGCCATGAGGACAAAAAACATTTTGAGGAGCAACAGTCATCACAAAACCTTCTATCAGCAA 60 TACGATGAGGACAAATATGATTTTGAGGAGCAACAGTCATCACGAACACTTCTTCAGCAA 60	
kob.ell	TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTCATCACCAATCTCCTTTCAGCAA 60 TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTCATCACCAATCTCCTTTCAGCAA 60	
kob.meg	TACCATGAGGACAAATATCCTTCTGAGGAGCGACAGTCATCACTAATCTCCTTTCAGCAA 60	
red.aru	TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTTATCACTAATCTTCTCTCAGCAA 60 TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTTATCACTAATCTTCTCTCAGCAA 60	
red.ful	TACCATGACGACAAATATCCTTCTGACGAGCAACAGTTATCACTAACCTTCTCACCAA 60 TGCCATGGCGACAAATATCCTTCTGAGGAGCAACAGTTATCACTAACCATTCTACTACGAA 60	
neo.mos	TOCCATOGOGICAAATATCCTTCTGAGGAGCAACAGTCATCACCAATCTACTACTCAGCAA 60 TGCCATGGGGACAAATATCCTTCTGAGGAGCAACAGTCATCACCAACCTTCTCTCAGCAA 60 TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTTATCACCAACGTTCTCTCAGCAA 60	
pel.cap	TACCATGAGGACAAATATCCTTC ISAGGAGCAACAC I SATCACTAACCTCCTCTCAGCAA 60 TACCATGAGGACAAATATCTTTCTGAGGACAACACTTATCACTAACCTCCTCTCAGCAA 60	
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mai.kir	TGCTATGAGGAGAAATATGCTTTTGAGGAGGAACACTATGAGTAATGTGGTGTCAGGAA 60 TACCATGGGGAGAAATATGCTTTTGAGGAGGAACAGTGATGATGAGTGATGGTGTGAGGAA 60	
sap.mel	TACCATGGGGACAATATTCTTTGAGGACIAACAC TA LA TAA TGAGCGTCTCAGCAA 59 TACCATGAGGACTACTATTATTA SAAGCAGGACTTCTTCAGCAATAGGACTACTAGGACTACTAGGACTAGGACTAGGACTAGGACTAGGACTAGGACTAGGACTAGGACTAGGACTAGGACTAGGACTAGGACTAGAATAGACTAGAGACTAGAATAGACTAGAATAGAATAGACTAGAATAGACTAGAATAGACTAGACTAGAATAGACTAGAATAGAATAGAATAGAATAGAATAGACTAGAA	
gaz gaz	TACCATGACGACAATATGTTTTTTTTAGUAGUAGUAGUAGUAGUAGATAGTGATCAGCAAATAGTGACGACTACTGAGCAAATATGATGAGCAAATATGAGCAAATATGAGCAAATATGAGCAAATATGAGCAAATATGAGCAAATATGAGCAAATATGAGCAAATATGAGCAAATATGAGCAAATATGAGCAAATATGAGCAAATATGAGCAAATATGAGCAAATAGTGAGCAAATAGAGAAATAGAGAAATAGAGAAATAGAGAAATAGAGAAATAGAGAAATAGAGAAATAGAGAAATAGAGAAATAGAGAAATAGAGAAATAGAGAAATAGAGAAATAGAGAAATAGAGAAATAGAGAAATAGAGAAATAGAGAAATAAAAATAGAAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAAATAGAAAAATAGAAAATAGAAATAGAAAATAGAAAATAGAAAAAA	
ant.ame	TACTATTAGGACAATATTATTATTAGGAGAA. 60 TTCATTAGTAATATTACTTAGGAGAA. 60 TTCATTAGGACAAATATTATTAGGAGAA. 60	
hyd.ine	TTECATTAGGA:AATATTATTE: GAUGAGIAM 100.1 A. TACTACTTECTTTCAGGAA 50 TACGATGAGGACAAATATGATTTTTGAGGAGGAAGAGTGATGATGAGGTGGT	
munimun alcialo	TACCATGAGGAGAGATATTA TITTTAGGGAGAGAGAGAGATTA ITTAACCTTCTTTTAGGAA 40 TACCATGAGGAGAGATATTA TITTTAGGGAGAAGAGAGAGAGAGAGAGAGAGAGAGAA 40	
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con.tau	TATTACTAATTCTAGCCCTAATACTACTAGTACTATTCGCGCCCGATTTACTTGGAGACC	350
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lage.alb	TACTTTTAATCCTAACCTTACTAGGACTAACCCTATTTAGGCGGGACCTACTAGGAGATG 350
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sota.flu	TACTCCTAATCCTGACCCTACTAGCACTAACCCTATTCACCCCCGACCTACTAGGAGATC 350
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Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593689-1224-27770

Query-

(328 letters)

Database: Sequences from complete mitochondrial genomes 129 sequences; 3,164,247 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAOS

Taxonomy reports

Distribution of 80 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments
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Sequences produci	ng significant alignments:	(bi	ts) '	Value
	complete denome	365	e-10	1
ref NC 001700.1	Felia catus mitochondrion, complete genome	198	1e-5	ı
ref[NC_001325.1]	Phoca vitulina mitochondrion, complete genome	190	46-4	9
ref NC 002008.1	Canis familiaris mitochondrion, complete g	180	3e-4	5
ref NC 001602.1	Halichoerus grypus mitochondrion, complete	176	5e-4	5
ref[NC_000884.1]	Cavia porcellus complete mitochondrial genome	155	2e-4	
ref NC 001808.1	Ceratotherium simum mitochondrion, complet	153	8e-31	3
ref NC 001892.1	Myoxus glis mitochondrion, complete genome	1,5,1	3e-3	7
ref NC_001788.1	Equus asinus mitochondrion, complete genome	149	1e-3	
TOF NC 002073.1!	Orycteropus afer complete mitochondrial ge	141	3e-3-	
Tef NC 001821.1	Dasypus novemcinctus mitochondrion, comple	135	2e-3	
re NC 001779.1	R.unicornis complete mitochondrial genome	133	7e-3	
ref NC 001569.11	Mus musculus mitochondrion, complete genome	125	2e-2	
Tef NC 000889.11	Hippopotamus amphibius mitochondrion, comp	125	2e-2	
ref NC 001640.1	Equus caballus mitochondrion, complete genome	123	7e-2	
== E NC 001794.1	Macropus robuscus mitochondrion, complete	121	3e-2	
ref NC 000845.1	Sus scrofa mitochondrion, complete genome	121	3e-2	
res NC 001665.1	Rattus norvegicus mitochondrial genome	121	3e-2	
ref NC 001567.1	Bos taurus mitochondrion, complete genome	$\frac{117}{117}$	4e-2	
ref NC 001643.11	Pan troglodytes mitochondrion, complete ge	109	1e-2	
ref NC 001941.1	Ovis aries mitochondrion, complete genome	103	7e-2	
ref NC 002391.11	Talpa europaea mitochondrion, complete genome	103	7e-2	3
ref NC 001913.1	Oryccolagus cuniculus mitochondrion, compl	101	3e-2	2
Tef NC 001644.1	Pan paniscus mitochondrion, complete genome	99	4e-2	1
ref NC 001807.2	Human mitochondrion, complete genome Balaenoptera musculus mitochondrion, compl	98	4e-2	1
ref NC 001601.1	Artibeus jamaicensis mitochondrion, comple	95	2e-2	3
ref NC 002009.1	Gorilla gorilla mitochondrion, complete ge	9.2	2e-1	€
ref NC 001645.1	Balaenoptera physalus mitochondrion, compl	90	1e-1	
ref NC 001321.1	Didelphis virginiana mitochondrion, comple	30	9e-1	5
ref NC 001610.1	Hylobates lar mitochondrion, complete genome	70	9e-1	3
ref NC 002082.11	Crossostoma lacustre mitochondrion, comple	70	9e-1	
ref NC 001727.1	Latimeria chalumnae mitochondrion, complet	<u> 58</u>	4e-1	
Tef NC 001804.1	Vidua chalybeata mitochondrion, complete 9	<u>56</u>	1e-1	
TEE NC 000880.1	Corvus frugilegus mitochondrion, complete	<u>_64</u>	6e-1	
ref NC 002069.1	Chalonia mydas mitochondrial DNA, complete	<u> 52</u>	2e-1	
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ref NC 000890.11	Mustalus manato mitochondrion, complete 95	_60	9e-1	
ref NC 001323.1	Callus callus mitochondrion, complete genome	<u> 50</u>	9e-1	
ref NC. 002079.1	Carageius auratus mitochondrion, complete	<u>_53</u>	1e-0	
ref NC 000934.1	torodonea africana mitochondrion, complete	<u> 56</u>	1e-0	
ref NC 000878.1	Falco peregrinus mitochondrion, complete 9	<u>56</u> 56	1e-0	
ref NC 000846.11	Rhea americana mitochondrion, complete genome	54	5e-0	
ref NC 002196.1	Ciconia boyciana mitochondrion, complete g	54	5e-0	
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ref NC 002083.1	Pongo pygmaeus abelii mitochondrion, compl	52	2e-0	
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NC 000884	14777	tcctaccacacaaa.	11777
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NC 000889 NC 001540 NC 001794 NC 000845 NC 001665	14718 14734 14730 14462 15888 14670	t.atg.g.g.catctcc	14744 14777 14793 14789 14475 15947 14729 15119
NC 000889 NC 001640 NC 001794 NC 000845 NC 001665 NC 001567	14718 14734 14730 14462 15888 14670 15060	t.atg.g.g.catctccaataactactaaaacaa	14744 14777 14793 14789 14475 15947 14729 15119
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NC 000934 14693	E	14277
NC 000878 14264	c.aa	14246
NC 000846 14235		14189
NC 000846 14187	***	15932
NC 001960 15930	***	14833
NC 001778 14823		14184
NC 001953 14170	c	15122
NC 001770 15120	•••	
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NC 001569 14745	gcat.ccaattgtgtgtgt	14837
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NC 001643 14771	cc	14824
NC 001941 14765		14814
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MC 001141 13004		15651
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NC 00100	2 1401	4	14893
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NC 00178			14853
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NC 00182	1 1483	7tt	14866
NC 00177	<u>9</u> 1484	4	14827
		5t	14860
NC 00088	9 1483	8tgc	
NC 00164	0 1485	4tttc	14876
NC 00164	15089	5	15098
NC 00179	14850	Jttt	14967
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NC 00166	14790	3 · P · P · P · .	14806
NC 00156	7 15180)tgct	15239
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NC 001643	14831		14853
NC 001941	14875	itct	14847
NC 001347	14841		14857
NC 00131	14937	· · · · · · · · · · · · · · · · · · ·	14854
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MC GOTAGE	1 1/015		14835
NC 002003	1/075		14863
NC 001843	16770	C	15295
NC 001321	1/0/2		14865
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NC 000345	16392	F F .CC	16421
NC 002193	14867		14895
NC 001953			14293
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NC 002008			14969
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NC 002078		d	-
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NC 001567		agccs.cacc	
NC 001313			492
NC 001644		actc.cta	.5532
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NC 001904			5108
NC 000985		, a., c., c., c., c., c., c., c., c., c., c	.50L7 .6507
NC 002195			
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NC 001008	447/U 14#47	c	
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NC 001172	14754	1177	

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NC 001779 308		. 3094
NC 000845 161	28ca	16144
NC 001911 1490		14980
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NC 001807 155	33c	15560
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NC 002003 149.	55 .gcac	14974
MC GOTOAS TAN	53cgca	14990
MC 001910 1436	53	14972
NC 002082 149	53e	
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NC 001951 144	e	24437

Database: Sequences from complete mitochondrial genomes Posted date: Jun 28, 2000 10:56 AM Number of letters in database: 3,164,247 Number of sequences in database: 129

Lambda 1.37 0.711 1.31

Gapped mbda K H 1.37 0.711 Lambda 1.31

Matrix: blastn matrix:1 -3 Gap Penalties: Existence: 5, Extension: 2 Number of Hits to DB: 788

Number of Sequences: 129 Number of extensions: 788

Number of successful extensions: 168 Number of sequences better than 10.0: 77

length of query: 328

length of database: 3,164,247 effective HSP length: 15

effective length of query: 313 effective length of database: 3,162,312

effective search space: 989803656

effective search space used: 989803656

T: 0 A: 30

X1: 6 (11.9 bits) XZ: 15 (29.7 bits)

S1: 12 (24.3 bics)

SZ: 14 (28.2 bits)

BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593400-28182-3122

Query-

(328 letters)

Database: nt

807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQS

Taxonomy reports

Distribution of 50 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments	
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Score
                                                                                                (bica) Value
 Sequences producing significant alignments:
                                                                                               603 e-170
gb[AY005809.1] Panthera pardus cytochrome b gene, partial c...
                                                                                               527 e-147
gb|AF053054.1|AF053054 Panthera tigris sumatrae isolate Sul...
gb|AF053053.1|AF053053 Panthera tigris tigris isolate 87 mi...
gb|AF053050.1|AF053050 Panthera tigris corbetti isolate C2 ...
                                                                                               527 e-147
                                                                                               476 e-132
                                                                                               476 e-132
gb/AF053049.1/AF053049 Panthera tigris corbetti isolate Cl ...
                                                                                               450 e-127
gb/AF053025.1/AF053025 Panthera tigris tigris isolate 89 Cy...
                                                                                               450 e-127
gb[AF053024.1[AF053024 Panchera tigris tigris isolate 88 cy...
                                                                                               450 e-127
gb[AF053023.1[AF053023 Panthera tigris tigris isolate B7 cy...
                                                                                               450 e-127
gb/AF053022.1/AF053022 Panthera tigris tigris isolate 86 cy...
gb|AF051021.1|AF051021 Panthera tigris tigris isolate BS cy...
                                                                                               460 e-127
Gb/AF053018.1/AF053018 Panthera tigris tigris isolate 82 cy...
                                                                                               450 e-127
GD | AF053018 1 | AF053018Panthera tigris tigris 1solate 82 Cy...GD | AF053051 1 | AF053051Panthera tigris corbetti isolate C3 ...GD | AF053048 1 | AF053048Panthera tigris sumatrae isolate Su1 ...GD | AF053047 1 | AF053047Panthera tigris sumatrae isolate Su7 ...GD | AF053045 1 | AF053045Panthera tigris sumatrae isolate Su6 ...GD | AF053044 1 | AF053044Panthera tigris sumatrae isolate Su5 ...GD | AF053042 1 | AF053042Panthera tigris sumatrae isolate Su1 ...GD | AF053041 1 | AF053041Panthera tigris sumatrae isolate Su2 ...GD | AF053040 1 | AF053040Panthera tigris sumatrae isolate Su2 ...GD | AF053040 1 | AF053040Panthera tigris sumatrae isolate Su2 ...
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gb AF053040.1 AF053040 Panthera tigris sumatrae isolate Sul...
                                                                                               452 e-125
cb/AF053039.1/AF053019 Panthera tigris altaica isolate 515 ...
                                                                                               452 e-125
gb/AF053038.1/AF053038 Panthera tigris altaica isolate $14 ...
                                                                                               452 e-125
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gb|AF053037.1|AF053037 Panthera tigris altaica isolate S13 ...
panthera tigris altaica isolate S12 ...

ph AF053036.1 | AF053036

panthera tigris altaica isolate S12 ...

ph AF053034.1 | AF053034

panthera tigris altaica isolate S10 ...

ph AF053033.1 | AF053031

panthera tigris altaica isolate S3 c...

ph AF053032.1 | AF053031

panthera tigris altaica isolate S7 c...

ph AF053031.1 | AF053031

panthera tigris altaica isolate S7 c...

ph AF053031.1 | AF053031

panthera tigris altaica isolate S7 c...
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cb|AF053031.1|AF053031 Panthera tigris altaica isolate S6 c...
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GD|AF053030.1|AF053030 Panthera tigris altaica isolate S5 c...
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gb|AF053023.1|AF053028
gb|AF053027.1|AF053027
gb|AF053026.1|AF053026
panthera tigris altaica isolate Si c...
panthera tigris tigris isolate Si c...
panthera tigris tigris isolate Si c...
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444 e-122
gb|AF053019.1|AF053019 Panthera tigris tigris isolate B3 cy...
gb|AF053043.1|AF053043 Panthera tigris sumatrae isolate Su4...
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                                                                                               440 e-121
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377 e-102
dbilAB004238.1|AB004238 Felis catus mitochondrial DNA for c...
dbi[A3004237.1[A3004237 Felis catus mitochondrial DNA for c...
emb|X82296.1|MIFDCYTB F.domesticus mitochondrial cytochrome...
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165
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276
46-70
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76-56
FEINC 001700.11 Felis carus mitochondrion, complete genome
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gb!AF125144.1|AF125144 Chrotogale owstoni cytochrome b gene...
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                                                                                               245
gb/AF125149.1/AF125149 Viverta tangalunga cytochrome b gene...
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AF051051 487
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AF051049
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AF051025
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AF053024
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AF051012 487
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AF051031
                      467
AFOSJOLS
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AF751951
AF953949
               487
AF751947
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AF053028	487	546
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AF053026	487	546
AF053020	487	
AF053019	487	
AF053043	487	
<u> X82301</u>	487	
AF053052	487	546
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AF125144	357	
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<u> AF154975</u>		
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A3051237 AF125149 Cmpseq_0 AY005809 AF053054	487 357 61 99 547	ttcatccttccatttatcatctcagctctagcagcagtccacctcctattccttcacgag 120
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AF051052	547		
X83300	547	aaa	606
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A3004237	547		606
X82296	547	tctcattata	15643
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U20753	15584	t	476
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AF154975	547	tgtgattt	606
AB051237	547	cgaaa	476
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AF053045	667	g,,,a,c,,,,,a,c,,,,,a,c,,,,,a,c,,,,,a,c,,,,,a,c,,,,a,c,,,,a,c,,,,a,c,,,,a,c,,,,a,c,,,,a,c,,a,c,,a,c,,a,c,,a,c,,a,c,,a,c,,a,c,,a,c,,a,c,,a,c,,a,c,,a,c,,a,c,,a,c,a,a,c,a,a,c,a,a,c,a,a,c,a,a,c,a,a,c,a,a,c,a,a,a,c,a	726
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AF053019	667		725
AF053043	667		726
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AY005809	279		785
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AF125144	657	C	
	787	⊂aa	803
AF154975			803
AB051237	787	caa	664
AF125149	657	C	004
WE TANK			

Database: nt

Posted date: Mar 2, 2001 12:20 AM Number of letters in database: 2,863,827,895

Number of sequences in database: 807,597

Lambda K H 1.37 0.711 1.31

Gapped

Lambda K H

52: 19 (38.2 bits)

1.37 0.711 1.31

Matrix: blastn matrix:1 -3 Gap Penalties: Existence: 5, Extension: 2 Number of Hits to DB: 460542 Number of Sequences: 807597 Number of extensions: 460542 Number of successful extensions: 22671 Number of sequences better than 10.0: 6487 length of query: 328 length of database: 2,863,827,885 effective HSP length: 20 effective length of query: 308 effective length of database: 2,847,675,945 effective search space: 877084191060 effective search space used: 877084191060 T: 0 A: 30 X1: 6 (11.9 bits) X2: 15 (29.7 bits) S1: 12 (24.3 bits)

WO 02/077278 71 PCT/IN01/00055

Table 5. Reference animals and the allocated code numbers included in the study

SN	I. Code number	Name of the animal	Zoological name
1	bhz25t	Indian tiger	Panthera tigris tigris
2	bhz26t	Indian tiger	Panthera tigris tigris
3	bhz30t	Indian tiger	Panthera tigris tigris
4	bhz45t	Indian tiger	Panthera tigris tigris
5	bhz56t	Indian tiger	Panthera tigris tigris
6	bhz63t	Indian tiger	Panthera tigris tigris
7	bhz20wt	Indian white tiger	Panthera tigris bengalensis
8	bhz22wt	Indian white tiger	Panthera tigris bengalensis
9	bhz23wt	Indian white tiger	Panthera tigris bengalensis
10	bhz28wt	Indian white tiger	Panthera tigris bengalensis
11	gz11	Normal leopard	Panthera pardus
12	gz2l	Normal leopard	Panthera pardus
13	gz3l	Normal leopard	Panthera pardus
14	gz21cl	Clouded leopard	Neofelis nebulosa
15	gz22ci	Clouded leopard	Neofelis nebulosa
16	darz14sl	Snow leopard	Panthera unicia
17	darz15sl	Snow leopard	Panthera unicia
18	darz16sl	Snow leopard	Panthera unicia
19	sbz22al	Asiatic lion	Panthera leo persica
20	sbz38al	Asiatic lion	Panthera leo persica
21	sbz39al	Asiatic lion	Panthera leo persica
22	humsk	Human	Homo sapiens sapiens
23	chimss	Chimpanzee	Pan sp.

Table 6. Multiple sequence alignments of the cytochrome b sequences of reference animals with the sequence obtained from confiscated animal remain

	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGGCTTCCAC	50
sbz22al	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
s5:38al	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
sbz39al	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCCTGACACGATTCTTTGCCTTCCAC	60
adil.flesh	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCTTGACACGATTCTTTGCCTTCCAC	60
gzini	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCTTGACACGATTCTTTGCCTTCCAC	60
g=2nl	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCTTGACACGATTCTTTGCCTTCCAC	60
grinl	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bh=23wt	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bh=28wt	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bh=22wt	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bhz20wt	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bhz63t	TO A THOMAS OF A COMMUNICATION OF A CANTAGE	9.0
bhzsát	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bhz26t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bhz30t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bhz45t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bh=25t	THE THEORY OF A COMMONICATION OF THE PROPERTY	60
dz14sl	TGAATCTGAGGAGGCTTCTCAGTACACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC TGAATCTGAGGAGGCTTCTCAGTACACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
d:15sl	TGAATCTGAGGAGGCTTCTCAGTACACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC TGAATCTGAGGAGGCTTCTCAGTACACAAAGCCACCCTGACACGATTCTTTGCCTTTCCAC	60
dz16sl		60
gz21cl		60
gz22cl	TGAATCTGAGGAGGCTACTCAGTAGACAGCCCTACCCTTACACGATTCTTCACCTTCCAC TGAATCTGAGGAGGCTACTCAGTAGACAGCCCTACCCTTACACGATTCTTCACCTTCAC	60
chimss	TGAATCTGAGGAGGCTACTCAGTAGACAGTCCCACCCTCACACGATTCTTTACCTTTCAC	60
humsk	TOWN'T CRUMMAND COURSES AND	
- C C C w d w	TTC2TCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA	120
sbz22al	TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA	
sbz38al	TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGCACTCCACCTCCTGTTCCTCCATGAA	120
sbz38al sbz39al	TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG	120 120
sbz38al sbz39al adil.flesh	TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG	120 120 120
sbz38al sbz39al adil.flesh gz1nl	TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGCACTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG	120 120 120 120
sbz38al sbz39al adil.flesh gz1nl gz2nl	TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGCAGCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG	120 120 120 120
sbz38al sbz39al adil.flesh gz1nl	TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGCACTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG	120 120 120 120 120 120
sbz38al sbz39al adil.flesh gz1nl gz2nl gz3nl	TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGCACTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGCACTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG	120 120 120 120 120 120 120
sbz38al sbz39al adil.flesh gz1nl gz2nl gz3nl bhz23wt	TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGCACTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGCACTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG	120 120 120 120 120 120 120 120
sbz38al sbz39al adil.flesh gz1nl gz2nl gz3nl bhz23wt bhz28wt	TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGCACTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGCAGTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG	120 120 120 120 120 120 120 120
sbz38al sbz39al adil.flesh gz1nl gz2nl gz3nl bhz23wt bhz28wt bhz22wt	TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGCACTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGCAGTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG	120 120 120 120 120 120 120 120 120
sbz38al sbz39al adil.flesh gz1nl gz2nl gz3nl bhz23wt bhz24wt bhz22wt bhz20wt	TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGCACTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGCAGTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG	120 120 120 120 120 120 120 120 120 120
sbz38al sbz39al adil.flesh gz1nl gz2nl gz3nl bhz23wt bhz24wt bhz22wt bhz20wt bhz63t	TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG	120 120 120 120 120 120 120 120 120 120
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sbz38al sbz39al adil.flesh gz1nl gz2nl gz3nl bhz23wt bhz2awt bhz2cwt bhz2cwt bhz2cwt bhz2cot bhz5cc bhz5cc bhz5cc bhz4cc	TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG	120 120 120 120 120 120 120 120 120 120
sbz38al sbz39al adil.flesh gz1nl gz2nl gz3nl bhz23wt bhz2awt bhz2cwt bhz2cwt bhz2cwt bhz2cwt bhz2cwt bhz5cc bhz5cc bhz5cc bhz5cc bhz5cc bhz5cc bhz5cc bhz5cc bhz5cc	TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTTCCTCCATGAG TTCATCCTTCCATTTATCATCCTCCATGAGCAGCAGTCCACCTCCTATTTCCTCCATGAG	120 120 120 120 120 120 120 120 120 120
sbz38al sbz39al adil.flesh gz1nl gz2nl gz3nl bhz23wt bhz2awt bhz2cwt bhz2cwt bhz2cwt bhz2cot bhz5cc bhz5cc bhz5cc bhz5cc bhz3cc bhz3cc bhz4cc bhz2cc bhz2cc bhz2cc bhz2cc bhz3cc bhz2cc bhz3cc bhz3cc bhz4cc bhz2cc	TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAAGCCCTAGCAGCAGTCCACCTCCTATTTCCTCCATGAG TTCATCCTTCCATTTATCATCCTCCATGAGCAGCAGTCCACCTCCTATTTCCTCCATGAG	120 120 120 120 120 120 120 120 120 120
sbz38al sbz39al adil.flesh gz1nl gz2nl gz3nl bhz23wt bhz2awt bhz2cwt bhz2cwt bhz2cwt bhz2cwt bhz5cc bhz5cc bhz5cc bhz5cc bhz5cc bhz3cc bhz4cc bhz2cc dz14s1 dz15s1	TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCCAGCCCTAGCAGCAGTCCACCTCCTTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCCAGCCCTAGCAGCAGTCCACCTCCTTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCCAGCCCTAGCAGCAGTCCACCTCCTTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCCAGCCCTAGCAGCAGTCCACCTCCTTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCCAGCCCTAGCAGCAGTCCACCTCCTTATTCCTCCATGAG TTCATCCTTCCATTTATCATCCTCCATGACACTCCTTATTCCTCCATGAG	120 120 120 120 120 120 120 120 120 120
sbz38al sbz39al adil.flesh gz1nl gz2nl gz3nl bhz23wt bhz2awt bhz2cwt bhz2cwt bhz2cc bhz5cc bhz5cc bhz5cc bhz5cc bhz5cc bhz4cc bhz2cc dz14s1 dz15s1 dz16s1	TTCATCCTTCCATTTATCATCTCAGCCTAGCAGCAGTCCACCTCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCCACCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCCACCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCCACCCTAGCAGCAGTCCACCTCCTATTTCCTCCATGAG TTCATCCTTCCATTTATCATCCACCCTAGCAGCAGTCCACCTCCTATTTCCTCCATGAG TTCATCCTTCCATTTATCATCCACCCTAGCAGCAGTCCACCTCCTATTTCCTCCATGAGAGTCCACCTCCTATTCCTCCATTCCACCTACCACCTCCACCTACCACC	120 120 120 120 120 120 120 120 120 120
sbz38al sbz39al adil.flesh gz1nl gz2nl gz3nl bhz23wt bhz2awt bhz2cwt bhz2cwt bhz2cwt bhz5cc bhz5cc bhz5cc bhz5cc bhz5cc bhz4cc bhz2cc bhz1scc dz14sl dz15sl dz16sl gz2lcl	TTCATCCTTCCATTATCATCTCAGCCTAGCAGCAGTCCACCTCTGTTCCTCCATGAA TTCATCCTTCCATTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTTCCTCCATGAA TTCATCCTTCCATTTATCATCTCAGCCTTAGCAGCAGTCCACCTCCTATTTCCTCCATGAA TTCATCCTTCCATTTATCATCCTCAGCCTTAGCAGCAGTCCACCTCCTATTTCCTCCATGAA TTCATCCTTCCATTTATCATCCTCAGCCTTAGCAGCAGTCCACCTCCTTATTTCTTCCATCATGAA TTCATCCTTCCATTTATCATCCTCCACCTTAGCACCTTCCTT	120 120 120 120 120 120 120 120 120 120
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gz2nl	ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCCATTCCACCCA	133
gz3nl	ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA	130
bhz23wc	ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA	130
bhz28wt	ACAGGATCTÁACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA	130
bhz22wt	ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA	130
bhz20wc	ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA	180
bhz63t	ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA	180
bhz56t	ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA	180
bhz26t	ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCGCGTTCCACCCA	130
bhz30c	ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA	130
bhz45c	ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA	180
bh:25t	ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA	130
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dz15sl	ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA	130
d:16sl	ACAGGATCTAACAACCCCTCAGGAATAGTATTTCACTAGACAAAATATCACCCGTTCACCCG	130
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gz22cl	ACAGGATCCAATAACCCCTCAGGAATGGTATCCGATTCAGACAAAATCCCGTTCCACCCG	180
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gz3ml	TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC	240
bh:23wt	TACTACACAATCAAAGACATCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC	240
bhz29wt	TACTACACAATCAAAGACATCTIGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC	240
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bhz63c	TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC	240
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bhz26t	TACTACACATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC	240
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bhz45c	TACTACACATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC	240
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bhz20wt	GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA	300
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dz15sl	GTCCTATTCTCACCAGACCTATTAGGGGACGCCGATAACTACATCCCCGCCAACCCTCTA	300
dz16sl	GTCCTATTCTCACCAGACCTATTAGGGGACGCCGATAACTACATCCCCGCCAACCCTCTA	300
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gz22cl	GTTCTATTCTCCCCAGACCTACTAGGAGACCCTGACAATTACACTCCCGCCAACCCTCTA	300
chimss	ACACTATTCTCACCAGACCTCCTGGGCGATCCAGACAACTATACCCTAGCTAACCCCCTA	300
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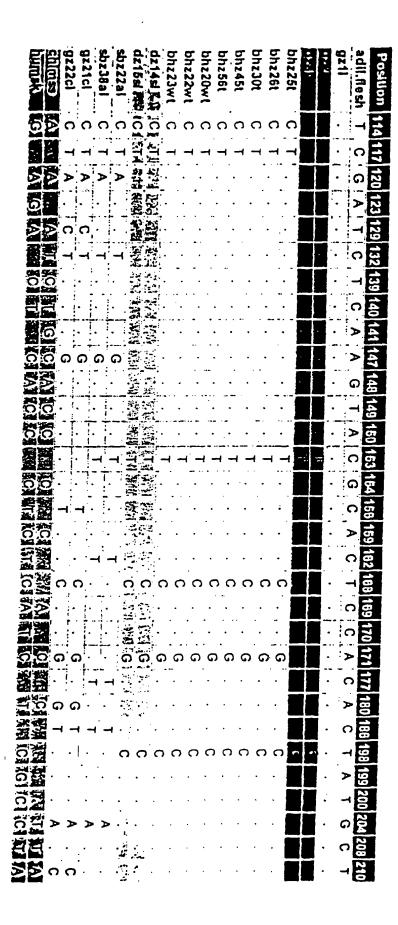


Table 7b

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Table 7c

Table 7d

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Table 8. Percent similarity matrix calculated by pair-vise comparisons of cytochrome b gene sequences revealed from 'adil.flesh' and different felids

			•								
	bhz20wt bhz25t	bhz25t	dz14si	humsk	chimss	sbz22al	gz1L	gzZL	023L	gz21cl	adil.flesh
bhz20wt		100	99.1	81.7	78.7	93.3	95.1	95.4	95.4	9.68	95.4
bhz25t	100		99.1	81.7	78.7	93.3	95.1	95.4	95.4	89.6	95.4
dz14si	99.1	99.1		81.4	78.4	93	94.8	95.1	95.1	89.3	95.1
humsk	81.7	81.7	81.4		6.98	9.62	81.1	80.2	80.2	79	81.4
chimss	78.7	7.8.7	78.4	86.9		7.87	79.6	78.7	78.7	76.8	79.9
sbz22ai	93.3	93.3	. 93	79.6	78.7		92.1	92.4	92.4	89	92.4
gz1L	95.1	95.1	94.8	81.1	9.62	92.1	100 794	98.5	98.5	89.3	7.66
gr2L	95.4	95.4	95.1	80.2	78.7	92.4	98.5		100	88.1	98.2
graf	95.4	95.4	95.1	60.2	78.7	92.4	98.5	100		88.1	98.2
g221cl	89.6	9.68	89.3	7.9	76.8	80	89.3	08.1	88.1		89.6
adil.flesh		95.4	95.1	81.4	79.9	92.4	2.60	98.2	98.2	89.6	

Table 10

BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984591695-10075-13605

Query-

1

(25 letters)

Database: nt

807,597 sequences: 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAOS

Taxonomy reports

Distribution of 500 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments	
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E. Score (bics) Value Sequences producing significant alignments: 50 2e-05 gb|AF231651.1|AF231651 Strongylura notata clone HB-82 cytoc...
gb|AF231650.1|AF231650 Strongylura notata clone HB-159 cyto... _50 2e-05 _50 2e-05 ref NC 002672.1 Dinornis giganteus mitochondrion, complete...
ref NC 002673.1 Emeus crassus mitochondrion, complete genome <u>5</u>0 2e-05 <u>50</u> 2e-05 qb/AF232015.1/AF232015Nothrotheriops shastensis cytochrome.502e-05gb/AF232013.1/AF232013Bradypus variegatus cytochrome b gen.502e-05 gb | AF232013.1 | AF232013Bradypus variegatus cytochrome b gen...502e-05gb | AY016015.1 | Emeus crassus mitochondrion, complete genome502e-05gb | AY016013.1 | Dinornis giganteus mitochondrion, complete g...502e-05gb | AY016014.1 | Dromaius novaehollandiae mitochondrion, part...502e-05gb | AF230167.1 | AF230167 | Bonasa umbellus cytochrome b (CYT3)502e-05gb | AF074594.1 | AF074594 | Baeolophus bicolor cytochrome b gene...502e-05gb | AY005210.1 | Poospiza melanoleuca isolate 3 cytochrome b ...502e-05gb | AY005209.1 | Poospiza melanoleuca isolate 2 cytochrome b ...502e-05gb | AY005208.1 | Poospiza melanoleuca isolate 1 cytochrome b ...502e-05gb | AY005204.1 | Poospiza fispaniolensis cytochrome b (cytb) gene, ...502e-05gb | AY005204.1 | Poospiza garleppi cytochrome b (cytb) gene, ...502e-05 gb | AY005203.1 | Poospital hispaniolensis cytochrome b (cytb)502e-05gb | AY005204.1 | Poospital garleppi cytochrome b (cytb) gene.502e-05gb | AY005203.1 | Poospital erythrophrys cytochrome b (cytb) gene.502e-05gb | AY005201.1 | Poospital bolivianal cytochrome b (cytb) gene.502e-05gb | AY005199.1 | Poospital alticolal isolate 2 cytochrome b (cytb) gene.502e-05gb | AY005198.1 | Poospital alticolal isolate 1 cytochrome b (cytb) gene.502e-05gb | AF155870.1 | AF155870 | Heterocephalus glaber cytochrome b (cytb) gene.502e-05gb | AF102099.1 | AF102099 | Criniferoides glaber cytochrome b (cytb) gene.502e-05gb | AF102099.1 | AF102099 | Criniferoides glaber cytochrome b (cytb) gene.502e-05gb | AF102095.1 | AF102099 | Criniferoides glaber cytochrome b (cytb) gene.502e-05gb | AF271065.1 | AF271065 | Mustelal ermineal specimen-voucher af1.502e-05gb | AF243857.1 | AF243857 | Strongylural notatal notatal cytochrome.502e-05gb | AF243856.1 | AF243856 | Strongylural notatal forsythial cytochrome.502e-05gb | AF306872.1 | AF306872 | Brachyramphus marmoratus haplotype M.502e-05gb | AF306871.1 | AF306871 | Brachyramphus marmoratus haplotype M.502e-05 | Elaphe | Obsoleta | Cytochrome | Dene, | C. | So | 2e-05 |
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Charalista	Larelista	Elaphe	Obsoleta	Cytochrome	Dene,	C.	So	2e-05	
Charalista	Larelista	Elaphe	Obsoleta	Cytochrome	Dene,	C.	So	2e-05	
Charalista	Larelista	Elaphe	Obsoleta	Cytochrome	Dene,	C.	So	2e-05	
Charalista	Larelista	Elaphe	Obsoleta	Cytochrome	Dene,	C.	So	2e-05	
Charalista	Larelista	Elaphe	Obsoleta	Cytochrome	Dene,	C.	So	2e-05	
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Charalista	Larelista	Elaphe	Obsoleta	Cytochrome	Dene,	C.	So	2e-05	
Charalista	Larelista	Elaphe	Obsoleta	Cytochrome	Dene,	C.	So	2e-05	
Charalista	Larelista	Elaphe	Obsoleta	Cytochrome	Dene,	C.	So	2e-05	
Charalista	Larelista	Cytochrome	Dene,	C.	So	2e-05			
Charalista	Larelista	Cytochrome	Dene,	C.	So	2e-05			
Charalista	Larelista	Cytochrome	Dene,	C.	So	2e-05			
Charalista	Larelista	Cytochrome	Dene,	C.	So	2e-05			
Charalista	Cytochrome	Dene,	C.	So	Cytochrome	Dene,	C.	So	2e-05
Charalista	Cytochrome	Dene,	C.	So	Cytochrome	Dene,	C.	So	Cytochrome

Table 9. Animals selected for validation of minimum P'S score for efficient amplification of DNA templates in PCR

SL.	Name	P. S/AFF	P. S/AFR	
1	Indian black buck (Antilope cervicapra)	97, 58	96, 54	
2	Sheep (Ovis	87, 53	96, 54	
3	Pig (Sus scrofa)	87, 52	87, 41	
4	Fresh water dolphin (Platanista gangetica)	86, 49	82, 47	

Sequences producing significant alignments:		ore ics)	E Value
gb[AF231651.1]AF231651 Strongylura notata clone HB-82 cytoc	50	2e-	
gb AF231650.1 AF231650 Strongylura notata clone HB-159 cyto	_50		
ref[NC 002672.1] Dinornis giganteus mitochondrion, complete	_50		_
ref[NC 002673.1] Emeus crassus micochondrion, complete genome	_ <u>5</u> ,0 _5,0		
gb[AF232015.1]AF232015 Nothrotheriops shastensis cytochrome gb[AF232013.1]AF232013 Bradypus variegatus cytochrome b gen	_50		
gb[AY016015.1] Emeus crassus mitochondrion, complete genome	50	2e-	
gb[AY016013.1] Dinormis giganteus mitochondrion, complete g	50		
gb/AY016014.1 Dromaius novaehollandiae mitochondrion, part	_50	2e- 2e-	
gb AF230167.1 AF230167 gb AF074594.1 AF074594 Baeolophus bicolor cytochrome b gene	_ <u>50</u> 50		
db AY005210.1 Poospiza melanoleuca isolate 3 cytochrome b	50	2e-	
gb AY005209.1 Poospira melanoleuca isolate 2 cytochrome b	50		
gb AY005208.1 Poospiza melanoleuca isolate 1 cytochrome b	50		
gb AY005205.1 Poospiza hispaniolensis cytochrome b (cytb)	<u>50</u>		
gb AY005204_1 Poospiza garleppi cytochrome b (cytb) gene gb AY005203_1 Poospiza erythrophrys cytochrome b (cytb) ge	50		
gb AY005Z01.1 Poospiza boliviana cytochrome b (cytb) gene,	50	2e-	05
chiayoo5199.1 Poospiza alticola isolate 2 cytochrome b (cy	_50		
qb AY005198.1 Poospiza alticola isolate 1 cytochrome b (cy	<u> 50</u>		
gb AF155870.1 AF155870 Heterocephalus glaber cytochrome b (gb AF189123.1 AF189123 Glyptotermes eukalypti cytochrome b	<u>50</u>		
gb AF189123.1 AF189123 Glyptotermes eukalypti cytochrome b gb AF102099.1 AF102099 Criniferoides leucogaster cytochrome	50	2e-	
gb AF102095.1 AF102095S1 Corythaixoides concolor cytochrome	50		
gb/AF271065.1/AF271065 Mustela erminea specimen-voucher AF1	<u>50</u> 50	2e-0	
cb AF243857.1 AF243857 Strongylura notata notata cytochrome cb AF243856.1 AF243856 Strongylura notata forsythia cytochr	50	2e-(
<pre>cb AF243856.1 AF243856 Strongylura notata forsythia cytochr ref NC 001567.1 Bos taurus mitochondrion, complete genome</pre>	50		
cb/AF306872.1/AF306872 Brachyramphus marmoratus haplotype M	50	2e-0	
gb[AF306871.1[AF306871 Brachyramphus marmoratus haplotype M	<u> 50</u>		
gb AF306870.1 AF306870 Brachyramphus brevirostris haplotype gb AF306869.1 AF306869 Brachyramphus brevirostris haplotype	<u>50</u>	2e-0	
gb AF306869.1 AF306869 Brachyramphus brevirostris haplotype gb AF306868.1 AF306868 Brachyramphus brevirostris haplotype	50	2e-0	
cb AF010406.1 AF010406 Ovis aries complete mitochondrial ge	50	2e-0	
gb[AF248662.1[AF248662 Gryllus campestris haplotype 2 cytoc	<u>50</u>	2e-0	
gb AF248661.1 AF248661 Gryllus campestris haplotype 1 cytoc gb AF096462.1 AF096462 Rhipidura albicollis cytochrome b ge	50	2e-0	
cb AF283644_1 AF283644 Elaphe obsoleta cytochrome b gene, C	50		
gb/AF283643.1/AF283643 Elaphe obsoleta cytochrome b gene, c	<u> 50</u>	2e-0	
gb AF283642_1 AF283642 Elaphe obsoleta cytochrome b gene, c	<u>50</u> 50	2e-0	
db AF283640.1 AF283640 Elaphe obsoleta cytochrome b gene, C	50	2e-0	
gb AF283639.1 AF283639 Elaphe obsoleta cytochrome b gene, c	_50	2=-0	
gb AF283637.1 AF283637 Elaphe obsoleta LSUMZ 45359 cytochro gb AF283636.1 AF283636 Elaphe obsoleta LSUMZ 44662 cytochro	<u>50</u> 50	2e-0	
gb[AF283636.1 AF283636 Elaphe obsoleta LSUMZ 44662 cytochro gb[AF283635.1 AF283635 Elaphe obsoleta LSUMZ 40443 cytochro	50	2e-0	
qb(AFZ83634.1(AFZ83634 Elaphe obsoleta LSUMZ 44335 cytochro	50	2e-0	
gb AF283633.1 AF283631 Elaphe obsoleta LSUMZ 42624 Cytochro gb AF283632.1 AF283632 Elaphe obsoleta LSUMZ H1911 cytochro	<u> 50</u>	2=-0 2=-0	
gb AF283632.1 AF283632 Elaphe obsoleta LSUMZ H1911 cytochro gb AF283631.1 AF283631 Elaphe obsoleta LSUMZ 41197 cytochro	50	2e-0	
qb AF283630.1 AF283630 Elaphe obsoleta LSUME 41189 cytochro	50	22-0	
gb AF283629.1 AF283629 Elaphe obsoleta LSUMZ 41188 cytochro gb AF283628.1 AF283628 Elaphe obsoleta LSUMZ 41187 cytochro	<u>50</u>	2e-0	
db AF283628.1 AF283628 Elaphe obsoleta LSUMZ 41187 cytochro db AF283627.1 AF283627 Elaphe obsoleta LSUMZ 41186 cytochro	50	2=-0	5
qb AF283626.1 AF283626 Elaphe obsoleta LSUMZ 40943 cytochro	50	2e-0	
95 AF283625.1 AF283625 Elaphe obsoleta LSUMZ 17499 cytochro 95 AF283624.1 AF283624 Elaphe obsoleta LSUMZ 44480 cytochro	<u>50</u>	2e-0 2e-0	
gb AF283624.1 AF283624 Elaphe obsoleta LSUMZ 44480 cycochro gb AF283623.1 AF283623 Elaphe obsoleta LSUMZ 44451 cycochro	50	2-0	5
qb[AF28]622.1[AF28]622 Elaphe obsoleta LSUM2 40444 cytochro	50	Ze-0	
gb AF283621.1 AF283621 Elaphe obsoleta LSUMZ 19925 cytochro gb AF283620.1 AF283620 Elaphe obsoleta LSUMZ 19163 cytochro	50 50	2e-0	
chiafraj619.1[AF28]619 Elaphe obsoleta LSUM239162 cytochrom	50	2=-0	5
db[AF28]618.1[AF28]618 Elaphe obsoleta LSUMZ H15876 cytochr	20	Ze-01	
qb AF283617 1 AF283617 Elaphe obsoleca GSUM2 HIS892 cytochr	<u>50</u>	Ze-0	
db AF283615.1 AF283615 Elaphe obsoleta LSUME HIS870 cytochr	<u> 52</u>	24.0	5
gblaf781614 11Af781614 Elaphe obsoleta LSUMZ H15887 cytochr	50	₹= -0°	5
dblAF281611 11AF281611 Elaphe obsoleta LSUM2 H15888 cycoche	_57	5 = · 0.	,

	Elaphe obsoleta LSUMZ H15884 cytochr	50	2e-05
gb[AF283612.1]AF263612	manha checleta LSUME H15031 Cytochr	50	2e-05
9h AF283611.11AF283611	checlera LSUMZ H15030 Cytochi	_50	2e-05
gb AF283610.1 AF283610 gb AF283609.1 AF283609	minho obsoleta CAS 169468 CYECCETOM	50	2e-05
gb[AF283608.1]AF283608	Plant charlers LSUME H14782 Cytocht	_50	2e-05
95 AF281607.1 AF283607	Planta checiera LSUME H14781 Cytothe	_50	2e-05
95 AF283606.1 AF283606	Flanks charleta LSUME H14724 Cytochi	50	2e-05
95 AF283605.1 AF283605	Flanks obsoleta cytochrome b gene. C	<u>5</u> 0	2e-05
gb AF283604 . 1 AF283604	Flanke chacleta cytochrome b gene, C	_50	2e-05
95 AF283603.1 AF283603	Flanka chaoleta cytochrome b gene, C	50	2e-05
gb AF283602.1 AF283602	Flanke obsoleta LSUMI H3388 Cytochro	_50	2e-05 2e-05
gb AF283601.1 AF283601	Flanks chapleta LSUMZ H3385 cytochio	50	2e-05
gb AF283600.1 AF283600	Flanks obsoleta LSUMZ H3384 CytoChFO	<u> 50</u>	2e-05
gb AF283599 . 1 AF283599	Flanks bairdi LSUMI H3382 Cytochrome	50	2e-05
GD AF283598.1 AF283598	Flanks bairdi LSUMZ H3381 cytochrome	<u> 50</u>	2e-05
95 AF283597.1 AF283597	Flanks chanleta LSUMZ H3379 CYTOCREO	<u> 50</u>	2e-05
GD AF283596 . 1 AF283596	Flanks checleta LSUMZ 39616 Cycochro	<u>50</u>	2e-05
gb AF283595.1 AF283595	Elaphe obsoleta LSUMZ H3376 cytochro	50	2e-05
CD AF283594 . 1 AF283594	Elaphe obsoleta LSUMZ H3345 cytochro	50	2e-05
GD AF283593.1 AF283593	Elaphe obsoleta LSUMZ H3309 cytochro	50	2e-05
Gb AF283592.1 AF283592	Elaphe obsoleta LSUMZ H3306 cytochro	50	2e-05
GD AF283591.1 AF283591	Elaphe obsoleta LSUMZ H3276 cytochro	50	2e-05
gb/AF283590.1/AF283590	Elaphe obsoleta LSUMZ H3246 cytochro Elaphe obsoleta LSUMZ H3212 cytochro	50	2e-05
gb AF283589.1 AF283589	Elaphe obsoleta LSUMZ H3209 cytochro	50	2e-05
SD AF283588.1 AF283588	Elaphe obsoleta LSUMZ H3206 cytochro	50	2e-05
GD AF283587.1 AF283587	Elaphe obsoleta LSUMZ H3191 cytochro	50	2e-05
SD AF283586.1 AF283586	Elaphe obsoleta LSUMZ H3190 cytochro	50	2e-05
GD AF283585.1 AF283585	Elaphe obsoleta LSUMZ H3189 cytochro	_50	2e-05
CD AF283584 . 1 AF283584	Flanka chaoleta LSUMZ H3188 cytochro	_50	2e-05
cb AF283583 . 1 AF283583	tlanhe obsoleta LSUMZ H3186 Cytochio	_50	2e-05
gb AF283582.1 AF283582 gb AF283581.1 AF283581	Flance obsoleta LSUMZ H3169 Cytochio	50	2e-05
GD AF283580 . 1 AF283580	Flanke obsoleta CAS 203083 cytocarom	_50	2e-05 2e-05
gb AF283579.1 AF283579	Flanka obsoleta CAS 203079 cycochrom	<u> 50</u>	2e-05
GD AF283578.1 AF283578	Flanks obsoleta LSUMZ H2286 Cytochio	<u>50</u>	2e-05
GD AF283577.1 AF283577	Elaphe obsoleta CAS 208631 cytochrom	50	2e-05
Gb AF283576.1 AF283576	Elaphe obsoleta LSUMZ H2229 cytochro	50	2e-05
GD AF187030.1 AF187030	Rhinophylla pumilio isolate TK46001	50	2e-05
GD AF310052.1 AF310052	Poospira hispaneolensis cytochrome b Volatinia jacarina cytochrome b gene	50	2e-05
gb AF310046.1 AF310046	Deinagkistroden acutus cytochrome b	50	2e-05
GD AF171919.1 AF171919	Trimeresurus mucrosquamatus cych gen	50	2e-05
GD AF171897.1 AF171897	toolaius cyanopus cytochrome D (cyto	_50	2e-05
gb AF290174.1 AF290174 gb AF290173.1 AF290173	agelajus phoeniceus cytochrome D (Cy	<u>50</u> .	2e-05
GD AF290171.1 AF290171	Onicalus major cytochrome b (cyto)	50	2e-05
gb AF290170.1 AF290170	amblucatous holosericeus cytochrome	<u> 50</u>	2e-05 2e-05
gb AF290150.1 AF290150	volunialia lacarina cytochrome b (cyt	<u>50</u>	2e-05
95 AF176252.1 AF176252	pairbrodontomys zacatecae cytochrome	50	2e-05
GD AF176251 . 1 AF176251	Reithrodontomys zacatecae cytochrome	50	2e-05
gb AF163907.1 AF163907	Microtus manthognathus cytochrome b Microtus pinetorum cytochrome b gene	50	2e-05
GD AF163904.1 AF163904	Microtus ochrogaster cytochrome b ge	50	2e-05
95 AF163901.1 AF163901	Microtus miurus cytochrome b gene. C	50	2e-05
g5[AF163899.1[AF163899	mistarus californicus cycochrome 8 (_50	2e-05
95 AF163891.1 AF163891 95 AF163890.1 AF163890	wistorie abbreviatus cytochrome B (C	<u> 50</u>	2e-05
95 AF288524. 1 AF288524	nicochelve dussumieri isolate Germa	<u> 50</u>	2e-05 2e-05
GD AF288523.1 AF288523	nimochalva dussumieri isolate white	<u> </u>	2e-05
95 AF288522.1 AF288522	ningochalve dussumieri isolate ALCY	<u>50</u> 50	2e-05
GD AF123530 . 1 AF123530	pailonogon pyralophus cytochrome b (50	2e-05
gb AF123512.1 AF123512	Eubucco bourcierii Cucinkae cytochro	50	2e-05
95 AF206548 . 1 AF206548	Adolfus vauereselli cytochrome b gen Cymnorhina tibicen cytochrome b gene	5.7	2e-05
95 AF197857.1 AF197867	tiers auropaea cytochrome D gene, part	50	20-05
The second of the Cinese	los semicariostus mitochondrion, compi	50	Ze-05
ESTING 001943.11 Dasy	powercinctus mitochondrion, compie	50	2e-05 2e-05
95 AF141217.1 AF141217	namenta incombus country Tanzania Cy	<u> 50</u>	2e-05
GD AFTO1615. 1 AF201615	proceeding buchholic cyctchrome b gene	<u>50</u>	Ze-05
gb AF077920 . L AF077920	Bombus nevadensis cycochrome b gene Oreamnos americanus cycochrome b (cy	52	24-05
QD[AF1906]2,1[AF1906]2	-:	50	Ze-05
95 J01 194 11 80VMT 808	Cochlearius cochlearius cytochrome b	50	2=-05
951AF193830.11AF193830	••••		

PCT/IN01/00055

gb/U89181.1/CAU89181 Chlorostilbon aureoventris cytochrome	50	24-05
gb UR4171.1 AFUR9171 Asio flammeus cytochrome b (cytb) gene	္ဌင္တ	26-05
	50	
gb[AF217633.1[AF217813 Homoroselaps lacteus cytochrome b ge	50	
gb AF217822.1 AF217822 Hydrophis semperi cycochrome b gene	_	
qb AF217813.1 AF217813 Acanthophis antarcticus cytochrome b	_50	
<pre>gb[AF220i08.1]AF220408 Calliophis kelloggi cytochrome b (cy</pre>	_5.0	
gb[AF126430.1[AF126430 Ellobius fuscocapillus cytochrome b	50	
gb[AF090137.1]AF090137 Aythya americana mitochondrion. comp	<u>_50</u>	
gb AF059111.1 AF059111 Sarkidiornis melanotos cytochrome b	_50	2e-05
gb[AF059053.1 AF059053 Aix sponsa cytochrome b gene, partia	50	2e-05
gb[AF099308.1[AF099308] Icterus wagleri wagleri cytochrome b	5.0	
	50	2e-05
	_50	2e-05
gb AF099294.1 AF099294 Icterus gularis tamaulipensis cytoch		2e-05
gb/AF099293.1 AF099293 Icterus gularis gularis cytochrome b	50	
gb[AF160610.1]AF160610 Cricetomys emini Cemi636 cytochrome	_50	2e-05
gb AF036280.1 AF036280 Tragelaphus strepsiceros cytochrome	_50	2e-05
gb[AF036277.1]AF036277 Tragelaphus scriptus cytochrome b (c	<u>50</u>	
qb[AF036274.1] Tetracerus quadricornis cytochrome b (cytb)	<u>_50</u>	2e-05
qb AF194218.1 AF194218 Phrynosoma platyrhinos cytochrome b	<u>_ 50</u>	2e-05
gb AF194216.1 AF194216 Urosaurus ornatus cytochrome b gene,	50	2e-05
ref NC 002009.1 Artibeus jamaicensis mitochondrion, comple	50	2e-05
ref NC 001941.1 Ovis aries mitochondrion, complete genome	50	2e-05
ref[NC 000877.1] Aythya americana mitochondrion, complete g	50	2e-05
	50	2e-05
	50	2e-05
gb U27551.1 GCU27551 Grus canadensis tabida cytochrome b (c		2e-05
gb AF089058.1 AF089058 Quiscalus quiscula cytochrome b (cyt	<u>50</u>	2e-05
gb/AF089055_1/AF089055 Quiscalus major cytochrome b (cytb)	<u> 50</u>	2e-05
gb/AF089054.1/AF089054 Quiscalus lugubris cytochrome b (cyt	<u> 50</u>	
gb[AF089046.1]AF089046 Oreopsar bolivianus cytochrome b (cy	_50	2e-05
ab AF089042.1 AF089042 Molothrus badius cytochrome b (cytb)	_50	2e-05
gb AF089039.1 AF089039 Macroagelaius imthurmi cytochrome b	<u>_50</u>	2e-05
Gb AF089037.1 AF089037 Lampropsar tanagrinus cytochrome b (<u> 50</u>	2e-05
GD AF089026.1 AF089026 Gymnomystax mexicanus cytochrome b (_50	2e-05
gb/AF089025.1/AF089025 Gnorimopsar chopi cytochrome b (cytb	50	2e-05
cb AF089024.1 AF089024 Euphagus cyanocephalus cytochrome b	_50	2e-05
cb AF089023.1 AF089023 Euphagus carolinus cytochrome b (cyt	<u>50</u>	2e-05
cb/AF089021.1/AF089021 Dives warszwewiczi cytochrome b (cyt	50	2e-05
db AF089020.1 AF089020 Curaeus curaeus cytochrome b (cytb)	50	2e-05
gb AF089016.1 AF089016 Amblycercus holosericeus cytochrome	50	2e-05
gb[AF089013.1[AF089013 Agelaius xanthophthalmus cytochrome	50	2e-05
gb AF089012.1 AF089012 Agelaius xanthomus cytochrome b (cyt	50	2e-05
gb AF089008.1 AF089008 Agelaius phoeniceus sub-species phoe	50	2e-05
gb AF069006.1 AF089006 .Agelaius humeralis cycochrome b (cyt	50	2e-05
cb/AF089005.1/AF089005 Agelaius cyanopus cytochrome b (cytb	50	2e-05
gb[AF108696.1[AF108696] Scolomys juruaense cytochrome B (Cyt	50	2e-05
gb/AF108685.1/AF108685 Wiedomys pyrrhorhinos cytochrome B (50	2e-05
cb/AF108677.1/AF108677 Thomasomys oreas cytochrome B (cyt3)	50	2e-05
gb AF145511.1 AF145531 Melanoplus foedus Cytochrome b gene,	50	2e-05
gb AF145511,1 AF145511 Melanoplus angustipennis cytochrome	50	2e-05
gb/U89627.1 9MU89627 Bolitoglossa marmorea cytochrome b (cy	50	2e-05
q5 089623.1 89089623 Barrachoseps pacificus cycochrome b (c	50	20-05
q5 AF181470.1 AF181470 Okapia johnstoni Cytochrome b gene,	50	2e-05
qb AF084075_1 AF084075 Lagenorhymchus acutus cytochrome b g	5 C	2e-05
gb[090303.1[OMU90303] Ovibos moschatus cytochrome b (cytb) g	50	2=-05
ab U90302.1 OMU90302 Ovibos moschatus cytochrome b (cytb) g	50	2e-05
gb[U90301.1]OMU90101 Ovibos moschatus cytochrome b (cytb) g	50	2-05
q5 U90300.1 OMU90300 Ovibos moschatus cytochrome 5 (cyt5) g	50	Ze-05
gb[AF038883.1[AF03888] Deinagkistrodon acutus cytochrome b	50	26-05
qb[AF039268.1[AF039268] Agkiscrodon concorreix cytochrome b	50	2=-05
qb[AF039267.1]AF039267 Boa constrictor cytochrome b (cytb)	50	2=-05
gb S49215.1 S49215 apocytochrome b (sheep, domestic, Merino	50	2=-05
qb AF158698.1 AF158698 Geomys pinetis dytochrome b gene. co	50	2=-05
q5 AF158697.1 AF158692 Geomys bursarius jugossicularis cyto	50	Ze-05
qb AF068193.1 AF068191 Ithaginis cruentus cytochrome b (cyt	50	2e-05
q5/AF091629.1/AF091629 Ancilocapra americana cytochrome b (50	2-05
q5[AF02206].11 Tragelaphus screpsiceros cytochrome b (cyt5)	50	20-05
gb[AF022062.1] Tragelaphus derbranus cytochrome b (cytb) ge	_5_7	24-05
q5[AF032060.1] Hippocraque equinus cytochrome b (cytb) gene	<u> 57</u>	25-05
gb[AF022057.1] Tragelaphus oryx cytochrome b (cyth) gene, m.	30	22-05
35 AFILISOO . I AFILISON Lagenorhynchus acutus 180 ate LACUTA	37	205
gblaF111499 1[AF111499 Lagenorhynchus atutus Laciate LACUA)	59	25.05
	_	

gb[uc+645.1[LBuc9645 Loxocemus bicolor cycochrome b (cycb)	50	2e-05
Thinker of themselve Funeries notaeus cytochrome b (cytb) 5	<u>_50</u>	2e-05
This can a transcape Fundance murious eviochrome b (cyth) 9	_5 <u>0</u>	2e-05
This can alreason Friendles striatus fosteri CytoChrome	.50	2e-05
Turner of the weather Emigrates Striatus Strigilatus CytoChr	_50	2e-05
Thereares Inches Enjoyages Striatus Strigilatus Cytocat	_50	2e-05
This area alreaded Friends Striatus modfaniel Cytochiom	_50	2e-05
". iong , icourage) Emicrates strictus modfaniel CytoChiom	_50	2e-05
The state of the s	<u> 50</u>	2e-05
The same of the court of the same of the s	50	2e-05 2e-05
. Little and a language - Enigraphy (MTC) CVEOCREOME - LCYCAL - DTT.	<u> 50</u>	2e-05
qb U69764 1 EFU69764 Epicrates fordi cytochrome b (Cytochrome b)	<u>50</u> 50	2e-05
gb U69779.1 ECU69779 Epicrates centhria cytochrome b (cyto)	_50	2e-05
qb U69777.1 ECU69777 Epicrates cenchria cytochrome b (cyto)	50	2e-05
gb U69774.1 EAU69774 Epicrates angulifer cytochrome b (cytb gb U69774.1 EAU69774 Epicrates angulifer cytochrome b (cytb	50	2e-05
	50	2e-05
The state of the s	_50	2e-05
de la constrictor de la constrictor eviochiome b (cyta) ge	_50	2e-05
The same of the sa	_50	2e-05
The manager of manager when americana mitochondrion, comple	_50	2e-Q5
The case 11 Forest Chemidophorus tigris strain Isla Ang	_50	2e-05
Lincogget 113-2006267 Cremidophorus tigris strain Isla Smi	<u> 50</u>	2e-05
Cornochaetes taurinus cytochrome b 9	_50	2e-05 2 e -05
the manners at a region of a local about Dusel about Cycochicome D. S.	<u>50</u>	2e-05
Gb AF028821.1 AF028821 Damaliscus lunatus cytochrome J gen	<u>50</u> 50	2e-05
cb AF061340_1 AF061340 Artibeus jamaicensis mitochiniciat	_50	2e-05
cb AF076093.1 AF076093 Thalassarche impavida cytochrome b (cb AF076091.1 AF076091 Thalassarche carteri cytochrome b (c	50	2e-05
	50	2e-05
	50	2e-05
	50	2e-05
Throngons in process Garrodia nereis cytochrome b (cytb)	_50	2e-05
ilamanasa ilamanasa gregeria tropica cytochrome b (cytb)	_50	2e-05
blancaca ilamazosa nimedea dibsoni ovtochrome b (cytb)	50	2e-05
illargente illargente Diomedea enomonhora evtochrome b (cy	<u> 50</u>	2e-05 2e-05
GD/AF076048.1 AF076048 Diomedea Chionoptera Cytochrome D	<u>50</u> 50	2e-05
ab AF076047.1[AF076047 Diomedea antipodensis cytochrome D	50	2e-05
gb/UE3314.1/MSU83314 Micrastur semitorquatus cytochrome b (50	2e-05
cb/US3318.1/MEU83318 Microhierax erythrogenys cytochrome b cb/U37303.1/SAU37303 Synthliboramphus antiquus cytochrome b	50	2e-05
	50	2e-05
The same of the sa	50	2e-05
throng allegatione	_50	2e-05
The same all arrange Aerhia nyomaea cytochrome b gene, mito	_50	2e-05
	<u>50</u> 50	2e-05 2e-05
g5[U37087.1]ACU37087 Aethia cristatella cytochrome 5 gene,	50	2e-05
gb/U87525.1 HGU87525 Heterocephalus glaber cytochrome-b gen gb/U87524.1 HGU87524 Heterocephalus glaber cytochrome-b gen	50	2e-05
	50	2e-05
	50	2 - -05
There 7024 1 CTITI 7851 Saiga Satarica Cytochrome b gene, mito	<u> 50</u>	26-05
		2e-05 :
GD[U1786] 1 OAU1786] Oreamnos americanus cytochrome b gene	_50	
gb/U17861.1/OAU17861 Oreamnos americanus cytochrome b gene gb/U17862.1/OMU17862 Ovibos moschatus moschatus cytochrome	_50	29-05
gb[U17862.1 OMU17862 Ovide moschatus moschatus cytochrome	<u>50</u> 50	2e-05 2e-05
gb/U17862.1/OMU17862 Ovibos moschatus moschatus cytochrome gb/U17860.1/ODU17860 Ovis dalli cytochrome b gene, mitochon gb/U17859.1/OCU17859 Ovis canadensis cytochrome b gene, mit	<u>50</u> 50 50	2e-05 2e-05 2e-05 2e-05
gb U17862.1 OMU17862 gb U17860.1 ODU17860 gb U17899.1 OCU17853 gb U65274.1 TBU65274 Thomomys bottae cycochrome b gene, mit	<u>50</u> 50	2e-05 2e-05 2e-05 2e-05 2e-05
gb U17862.1 OMU17862 gb U17860.1 ODU17860 gb U17859.1 OCU17859 gb U55274.1 TBU65274 gb U65274.1 TBU65274 Thomomys bottae cytochrome b (cyto) ge	50 50 50 50 50 50	2e-05 2e-05 2e-05 2e-05 2e-05 2e-05
gb U17862.1 OMU17862 gb U17860.1 ODU17860 gb U17859.1 OCU17859 gb U55274.1 TBU65274 gb U65274.1 TBU65267 Thomomys bottae cytochrome b (cytb) ge gb U65260.1 TBU65260 gb U65260.1 TBU65260 gb U65260.1 TBU65260 gb U65260.1 TBU65260	50 50 50 50 50 50 50	2e-05 2e-05 2e-05 2e-05 2e-05 2e-05
gb U17862.1 OMU17862 gb U17860.1 ODU17860 gb U17859.1 OCU17859 gb U55274.1 T8U65274 gb U55267.1 T8U65267 gb U65260.1 T8U65260 gb U65260.1 T8U65260 gb U65101.1 PAU65101 gb U65101.1 PAU65101 gb U65101.1 PAU65101	50 50 50 50 50 50 50 50	2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05
gb U17862.1 OMU17862 gb U17860.1 ODU17860 Ovis dalli cytochrome b gene. mitochon gb U17859.1 OCU17859 Gb U55274.1 T8U65274 Thomomys bottae cytochrome b (cytb) ge gb U65267.1 T8U65267 Thomomys bottae cytochrome b (cytb) ge gb U65260.1 T8U65260 Thomomys bottae cytochrome b (cytb) ge gb U65101.1 PAU65101 Perognathus amplus cytochrome b (cytb) ge gb AFG14719.1 AFG14719 Capra aegagrus cytochrome b (cytb) ge	50 50 50 50 50 50 50 50 50	2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05
gb U17862.1 OMU17862 gb U17860.1 ODU17860 gb U17859.1 OCU17859 gb U55274.1 TBU65274 gb U65267.1 TBU65267 gb U65260.1 TBU65260 gb U65260.1 TBU65260 gb U65260.1 TBU65360 gb U65360.1 TBU65360	50 50 50 50 50 50 50 50 50 50 50	2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05
gb U17862.1 OMU17862 gb U17860.1 ODU17860 Ovis dalli cytochrome b gene, mitochon gb U17859.1 OCU17859 Ovis canadensis cytochrome b gene, mitochon gb U65274.1 TBU65274 Thomomys bottae cytochrome b (cytb) ge gb U65267.1 TBU65267 Thomomys bottae cytochrome b (cytb) ge gb U65260.1 TBU65260 Thomomys bottae cytochrome b (cytb) ge gb U65101.1 PAU65101 Perognathus amplus cytochrome b (cytb) gellafol4719.1 AF014719 Capra aegagtus cytochrome b (cytb) gellafol4719.1 Capra cytochrome b (cytb) gene, mitochrome b (cytb) gene, mito	50 50 50 50 50 50 50 50 50 50 50 50 50 5	2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05
gb U17862.1 OMU17862 gb U17860.1 ODU17860 Ovis dalli cytochrome b gene. mitochon. gb U17859.1 OCU17859 Gb U55274.1 TBU65274 Thomomys bottae cytochrome b (cytb) ge. gb U55267.1 TBU65167 Thomomys bottae cytochrome b (cytb) ge. gb U65260.1 TBU65160 Gb U65101.1 PAU65101 Gb AF014719.1 Capra caucasica cytochrome b (cytb) ge. gb AF014719.1 Capra cytindricornia cytochrome b (cytb) gene. gb AF014715.1 Capra cytindricornia cytochrome b (cytb) gene. gb AF014715.1 Capra cytindricornia cytochrome b (cytb) gb AF014715.1 Capra taleoneri cytochrome b (cytb) gb AF014715.1 Capra taleoneri cytochrome b (cytb) gb AF014715.1 Capra taleoneri cytochrome b (cytb)	50 50 50 50 50 50 50 50 50 50 50 50 50 5	2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05
gb U17862.1 OMU17862 gb U17860.1 ODU17860 Ovis dalli cytochrome b gene, mitochon gb U17859.1 OCU17859 Ovis canadensis cytochrome b gene, mitochon gb U65274.1 TBU65274 Thomomys bottae cytochrome b (cytb) ge gb U65267.1 TBU65267 Thomomys bottae cytochrome b (cytb) ge gb U65260.1 TBU65260 Thomomys bottae cytochrome b (cytb) ge gb U65101.1 PAU65101 Perognathus amplus cytochrome b (cytb) gellafol4719.1 AF014719 Capra aegagtus cytochrome b (cytb) gellafol4719.1 Capra cytochrome b (cytb) gene, mitochrome b (cytb) gene, mito	50 50 50 50 50 50 50 50 50 50 50 50 50 5	2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05

gb[AF03472F.1] Ovis dall: dall: dycochrome 5 (dycb) gene. m	50	2e-05
gh AF034717.11 Ovis ammon darwini cytochrome b (cytb) gene	<u> </u>	2e-05
gh[AF034717.]] Ovis ammon darwini cytochrome b (cyto) genetities gh[AF034714.][AF034724 Pantholops hodgsoni cytochrome b (cyto)	_50	2e-05
This energy of the profile the takes cytochrome of the desired	,50	Ze-05
gh U+4805 1 TMU94805 Trogon melanurus cytochrome b gene, mi	_50	2e-05
This was a little 4804 Troggn comptus cycochrome b gene, mito	_50	2e-05
Thirty and il Truly 4 803 Trogon viridis cytochrome b gene, mico	_50	2e-05
This moderner ilamonars, Sericossimba alborristata cytochrome	_50	2e-05
The second of the second suffices cytochrome b (Cy	<u> </u>	2e-05
This posting ! LAPONSTIR Lamprospica melanoleuca cytochrome D	_50	26-05
The control of a Fondaria Hemispingus atropileus cytochrome D	<u> 50</u>	2e-05
This constant largo 6226 Cypsnagra hirundinacea cytochrome b	_50	2e-05
The Toperas large 6215 Chlorophanes spita cytochrome b (cyt	<u>_5</u> 0	2e-05 2e-05
This moderna 112 months of the Chlorochrysa Calliparaea Cytochiome	50	2e-05
chiarone213.1/AF006213 Calochaetes coccineus cytochrone 5	<u>50</u>	2e-05
cb[AF006212.1[AF006212 Buthraupis montana cytochrome b toyeth	50	2e-05
emb AJ293419 1 RRU293419 Rupicapra rupicapra idpicapra ""	<u> 50</u>	2e-05
emb AJ293416.1 RPY293416 Rupicapra pyrenaica pyrenaica	50	2e-05
emb AJ293415 1 RPY293415 Rupicapra pyrehaica parva mirochon.	50	Ze-05
emb[AJ293+14.1]RPY293414 Rupicapra pyrenaica ornaca mitodino	50	2e-05
emb AJ293412 1 RRUZ93412 Rupicapra rupicapia iupicapia	50	2e-05
	_50	2e-05
	_50	2e-05
	_50	2e-05
Palmeria dolei cytochrome b (Cytb) S	_50	2e-05
This role 75 a 1 (2 TO 15758 Oreomystis mana cytochrome b (Cyto)	_50	2e-05
The state of the s	_50	2e-05 2e-05
The same of the sa	<u> 50</u>	2e-05
The same allowers of December of the property of the same of the s	<u>50</u>	2e-05
The transcare of Committee of the transcare of the transc	50	2e-05
gb/U83158.1/POU83158 Pelecanus onocrotalus cycochiome B gen	50	2e-05
gb[U83157.1 POU83157 Pelecanus onocrotalus cytochrome B gen	50	2e-05
cb/U83155.1/AAU83156 Anhinga anhinga cytochrome B gene, mit cb/U83155.1/AAU83155 Anhinga anhinga cytochrome B gene, mit	50	2e-05
	50	2e-05
	_50	2e-05
the transfer aleggranese stanks scalaris mitochondrial part	_50	2e-05
The state of the state of the scalaris mitochondrial part	_50	2e-05
Tanha longissima mitochondrial pa	<u>50</u>	2e-05 2e-05
13 777767; 1 F1027767; Flanke longissima mitochondrial pa	<u> 50</u>	2e-05
The total themselowed beginning novemblactus complete milescit.	_ <u>50</u> _ <u>50</u>	2=-05
emb[AJ388467.1]NBA388467 Nemachelius Dalbatutus minima	50	2e-05
emb[AJ388468.1[IME388468] Ictalurus melas mitchondrial cyt b emb[AJ388459.1[LDE388459] Leucaspius delineatus mitchondrial	50	2e-05
CHO 11.0 TO THE COURT	50	2e-05
	50	2e-05
This races a tiernasesa schilbe incermedius partial mitoch	<u> 50</u>	2e-05
This Tracers 1 EDEPASSIS FULTODIUS depressitostris partial	_50	Ze-05
This Tracert 11 morrasett Futropius depressirostris partial	<u>_50</u>	2e-05
emb[AJ745676.1[EDE245675 Eutropius depressirostris partial	_ <u>50</u> 50	2=-05
emb AJ245575.1 EDE245675 Eutropius depressirostris partial	<u>50</u>	20-05
emb AJJ45674 1 EDE245674 Eutropius depressirostris partial emb Y16884 3 MTRACOMPL Rhea americana complete mitochondria	50	2 e- 05
	50	Ze-05
This age 1 Try 1 ages That ages the melanophis melanophis C	_50	3e-05
The lineage of the large the large the chrysostoma cytochrome b	50	2e-05 2e-05
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gb]U48942 11PFU48342 Phoebetria tusca cytochrome b (cyto) 4	50	20-05
gb U48941 1 mGU48941 Macronectes giganteus cytochrome b (ty gb U48947 1 DEU48947 Diomedea exulans dabbenena cytochrome	50	2=-05
This gas ilmeragas promeded soomophora sanford: cycochiom	50	20-05
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luccede l'aguecede A theue D'entrostrie cytochrome b (cy	<u> 57</u>	2e-05 2e-05
dplaterou il vontered verpene opacarae chroqueme p (ches)	_50 _50	7e - 05
dp/055205 1/A0065205 Artibena opachina chrochiame p (chr)		

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gb[U66505.1]ALU66505 Artibeus lituratus cytochrome b (cytb)	50	2e-05
at the she illiffeens the their lamaicensis cytochrome of the	.50	20.00
Incent therent their tamaicensis cytochrome b (cyt	50	26-05
Thiseen liatureen twelfers intermedius cytochrome D (C)	50	2e-05
	<u>5</u> 0	2e-05
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	50	2e-05
qb/U66498.1/AFU66499 Artibeus fimbriatus cycochrome b (cytb	50	2e-05
gb[U63061.1[99U63061] Brachyramphus breviroscris cycochrome	50	2e-05
This ago 1 legis 1050 Brachyramphus brevitostis cytocarome		26-05
Thirdness righterings Arachyramphus breviroseris cycochiome	50	2e-05
THISTOGR TIRRIESDER Brachyramphus Drevitostris Cytochiome	_50	
Livering 1/6 tips 346 Scolomys juruaense cytochrome b (cyt-b	50	2e-05
This is a lice watering Cratogeomys gymnumus mitochondrial C	_50	2e-05
Livasta 1 MMT134572 Merachirus nudicaudatus cytochrome b 1	<u> 50</u>	2e-05
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	<u>.5</u> 0	2e-05
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	50	2e-05
gb Ll1904.1 CGYMTCYTBC Cratogeomys goldmani goldmani mitoch	50	2e-05
emb X94928.1 SPCYTB S.putorius mitochondrial DNA for cytoch	50	2e-05
cb/U46770.1/ARU46770 Anchus richardi cytochrome b gene, mit	50	2e-05
Thirdered Thankered Anthus berthelotti cytochrome b gene,	50	2e-05
Third clar ligginging Sciumis stramineus Cytochrome D Gene,		2e-05
Liviatos ilpenviatos p echwarzi micochondrial cyco gene,	<u> 50</u>	2e-05
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hivected ilempacyme C aura mitochondrial cych gene	_50	2e-05
Hallangerer 1/20035242 Pantodon buchholzi mitochondriai Cy	_50	2e-05
emb X60946.1 MITDC333 T. dorbignyi mitochondrial gene for c	_50	2e-05
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dbj[AB021095.1]AB021095 Cervus nippon yesoensis mitochondri dbj[AB021094.1]AB021094 Cervus nippon centralis mitochondri	50	2=-05
dhilanorider (lanorider Corvus nippon mageshimae mitochondr	50	2-05
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dri DB2192.1 CEUMTCELL Cervus hippon mitochondrial gene for	50	26-05
dhi[ABO:16ee 1]ABO:16ee Cervus elaphus scottcus micochondri	<u>_5</u> 0	26-05
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dbi[AB021096,1[AB021096 Cervus elaphus canadensis mirochond	ŠG	2e-05
Amilianing limbing Cames mindon mippon mitochondrial		2e-05
delignoring lighting compagnings pulchellus mitochonur	_50	2e-05
dbi[AB008539.1]AB008539 Dinocon semicarinatus mitochondrial	_5,0	
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emb[AJ010054.1]CPV010054 Capra pyrenaica (individual 11) mi	50	2e-05
- 1. tologed licovologed Capra Dyrenalca (individual 19/ mai)		2e-05
11 7010052 1 COVO10057 Canta pyrenaica (individual 9) mit	_50	
Target 1 Carra pyrenaica (individual 8) mit	_50	2e-05
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emb[AJ010048.1[CPV010048 Capra pyrenaica (individual),	50	2e-05
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Library alcohol C longitoseris micochondrial cytochrome	_50	
ilizadore ilorgore Canta ibex nubiana mitochondria: Cyt	<u>_50</u>	2e-05
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emb X95764.1 AAMC3 A.albertisi mitochondrial cytochrome b gene	43	8e-05
Lineares timesans aloes evenement (cyca) send	45	3e-04
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gb(AF157453.1(AF157463 Lepus corsicanus haplotype 3 cytochr	4.6	3e-04
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Tylogymis crocodilus clone HB-155 CY	-45	36-04
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db AF231656.1 AF231656 Tylosurus acus cytochrome b oxi	45	3e-04
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Alignments

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AJ000024	398		•
V00654	14911		
X56286	398	422	
L19718	398	425	
U27543	401	367	,
AB030025	343 169	193	1
<u>U18258</u> U18257	169	191	į
U18253	169		
U18250	169	191	
U17904	169		
D84202	398	422	
D82889	398		
D32195	243		
D12191	398	421	-
AB021098	398	427	_
AB021097	398 398		-
AB021095 AB021094	196		-
AB021092	198		
AB021091	196	42:	ľ

		422
AB001612	398	
D84205	398	
D84203	398	
D34636	398	
D34635	398	
D12198	243	
D32196	243	267
D32192	398	
AB021099	398	422
AB021096	398	422
AB021093	398	422
AB021090	398	422
AB008539	15302	15326
008300BA	398	422
L12763	260 .	284
L08032	401	425
L28941	398	422
L28917	398	422
AJ010056	269	293
AJ010054	269	293
AJ010051	269	293
AJ010052	269	293
AJ010051	269	293
AJ010050	269	293
AJ010030	269	293
AJ010043 AJ010048	269	293
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	407	431
<u> X95777</u> AJ009879	269	293
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U08946	303	327
U08945	303	327
U08944	303	327
U08941	303	327
U08940	303	327
X95775	303	327
X95774	303	327
X95764	303	327
AF040383	287	310
AF232023	400	
AF232022	400	
AF232021	400	
AF157466	322	344
AF157465	324	
AF157464	324	
AF157463	324	
AF157460	321	
AF231664	400	422
AF231663	400	422
AF231662	400	422
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AFZ31659	400	
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AF231656	400	422
AF231644	400	422
AF231639	_	
AF232019	400	422
AF232017	400	
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AF318564	345	
AF318563	345	
AF118562	344	366
AF318561	344	366
AF318560	344 344	166
AF118552 AF118558	344	366
AF118557	361	403
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AFILESIS	381	403
AFILESS1	361	

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AF318550 381	3
AF318549 381403	
AF318548 381	
AF238041 400	-
AF126272 400	
AF326271 400422	
AFJ26270 400	
AF326266 400	
AJ004340 302	
AJ004264 302	i
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Database: nt	
Posted date: Mar 2, 2001 12:20 AM	
Number of letters in database: 2,863,827,88	5
Number of sequences in database: 807,597	
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1.37 0.711 1.31	
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Gapped	
Lambda K H	
1.37 0.711 1.31	
Matrix: blastn matrix:1 -3	
Gap Penalties: Existence: 5, Extension: 2	
Number of Hits to DB: 39355	
Number of Sequences: 807597	
Number of extensions: 39355	
Number of successful extensions: 15066	
Number of sequences better than 10.0: 5706	
length of query: 25	
length of database: 2,863,827,885	
effective HSP length: 17	
effective length of query: 8	
effective length of database: 2,850,098,736	
effective search space: 22800789888	
effective search space used: 22800789888	
T: 0	

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T: 0 A: 30 X1: 6 (11.9 bits) X2: 15 (29.7 bits) S1: 12 (24.3 bits) S2: 16 (32.2 bits)

Table 11. BLAST analysis of primers 'mcb869' in nr database of NCBI. It demonstrates that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer.



BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593033-24247-14777

Query-

(26 letters)

Database: nt

807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the <u>BLAST FAQs</u>

Taxonomy reports

Distribution of 500 Blast Hits on the Ouerv Sequence

Mouse-over to show defline and scores. Click to show alignments	
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(bits) Value

Score

Sequences producing significant alignments:

<u>52</u> 6e-06 qb[AF189111.1[AF189111 Cryptotermes austrinus cytochrome b ... <u>52</u> 6e-06 gb|U86834.1|U86834 Phyllotis wolffsohni MSB 67270 cytochrom... 52 6e-06 qb[AF123633.1[AF123633 Perissocephalus tricolor cytochrome ... 52 6e-06 gb[AF123617.1|AF123617 Pipreola arcuata cytochrome b gene, ... 52 6e-06 gb|AF127202.1|AF127202 Hylopezus fulviventria cytochrome b ... gb|AF127194.1|AF127194 Grallaria guatimalensis cytochrome b... gb AF217828.1 AF217828 Aspidelaps scutatus cytochrome b gen... gb/AF160578.1/AF160578 Hypogeomys antimena Hant555 cytochro... gb|AF009931.2|AF009931 Archocentrus centrarchus cytochrome ...
gb|AF091629.1|AF091629 Antilocapra americana cytochrome b (... gb[AF034967.1] Sigmoceros lichtensteinii cytochrome b gene,... gb|AF038290.1|AF038290 Antechinus sp. cytochrome b gene, mi... gb | U07577.1 | AMU07577 Antechinus melanurus mitochondrion cyt...
gb | U81343.1 | CFU81343 Chelus fimbriata cytochrome b gene, mi... emb|AJ222681.1|ABCYTOB Alcelaphus buselaphus mitochondrial ...

gb|M99464.1|PNZMTCYTB Planigale sp. cytochrome b gene, comp...

emb|AJ225116.1|DNJ225116 Dryomys nitedula mitochondrial gen... gb | U25738.1 | PRU25738 Paradisaea raggiana cytochrome b gene,... 52 6e-06 52 6e-06 52 6e-06 gb U25736.1| PRU25736 Paradisaea rubra cytochrome b gene, mi... gb|U15202.1|SMU15202 Seleucidis melanoleuca mitochondrion c... qb|U15204.1|PR15204 Paradisaea raggiana mitochondrion cytoc... 52 6e-06 52 6e-06 emb|X56290.1|MIDDCYTB D.dama mitochondrion cyth gene for cy...
emb|X56286.1|MIAACYTBA A.americana mitochondrion cyth gene ... 52 6e-06 52 6e-06 46 3e-04 dbj|D88639.1|D88639 Anoa depressicomis mitochondrial DNA f... gb|AF119261.1|AF119261 Peromyscus maniculatus cytochrome b ... 45 3e-04 gb/AF123615.1/AF123615 Rupicola rupicola cytochrome b gene,... gb AF160603.1 AF160603 Apodemus sylvaticus Asyl588 cytochro... 45 3e-04 45 3e-04 gb|U62697.1|CCOLCYTB2 Charadrius collaris cytochrome b (cyt... 45 3e-04 gb|U62685.1|CBICCYTB2 Charadrius bicinctus cytochrome b (cy... gb AF022071.1 Madoqua guentheri cytochrome b (cytb) gene, ...
gb AF022070.1 Madoqua kirkii cytochrome b (cytb) gene, mit... 45 3e-04 45 3e-04 45 3e-04 gb U83317.1 PSU83317 Polihierax semitorquatus cytochrome b ...
gb U37293.1 CCU37291 Cephus columba cytochrome b gene, mitoc...
gb U37292.1 CCU37292 Cephus carbo cytochrome b gene, mitoc...
gb U37292.1 RMU37291 Brachyramphus marmoratus perdix cytoch... 45 3e-04 45 3e-04 45 3e-04 45 3e-04 45 3e-04 gb[AF082055.1]AF082055 Rupicola rupicola cytochrome b gene,... gb U72770.1 JMU72770 Jabiru mycteria cytochrome b gene, mit... 45 3e-04 qb/U07578.1|DCU07578 Dasycercus cristicauda mitochondrion c... 45 Je-04 SDIAFOIL908.1|GOCCCYTB1 Geopsittacus occidentalis cytochrom... 45 3e-04 46 3e-04 46 3e-04 emb|AJ004231.1|SBAJ4231 Sula bassana mitochondrial cyth gen...
emb|AJ004230.1|SBAJ4230 Sula bassana mitochondrial cyth gen... emb[AJ004229.1]SBAJ4229 Sula bassana mitochondrial cyth gen... emb|AJ004232.1|SBAJ4232 Sula bassana mitochondrial cyth gen... 45 Je-04 45 Je-04 gb[U88865.1] Pomacentrus sp. cytochrome b (cytb) gene, mito...]e-04]e-04 gb[U90001.1]MBU90001 Morus bassanus cytochrome b gene, mito...
gb[U63057.1]SMU63057 Brachyramphus marmoratus perdix cytoch... dbi|A3016404.1|A8016404 Rana porosa brevipoda micochondrial... dbj|AB036402.1|AB036402 Rana porosa brevipoda mitochondrial...
dbj|AB036400.1|AB036400 Rana porosa brevipoda mitochondrial... 3--04 34-04 3--04 dbj[AB0]6]98.1[AB0]6]98 Rana porosa porosa mitochondrial CN... 45 3=-04 qb|U19611.1|JMU19611 Jabiru mycteria cytochrome b gene, mit...
emb|X92519.1|HACYTB H.ampullatus cytochrome b gene (complet... 3=-04 3=-04 GB|[090]4.1|GAEMTC/TBA Galeocerdo cuvier mitochondrial cyto...
GB|[090]3.1|CPLMTC/TBB Carcharhinus porosus mitochondrial c... 3=-04 0.001 qb[AY015012.1] Crypturellus tataupa mitochondrion, partial ... 4 -4 0.001 qb[AF074591.1]AF074591 Petrochelidon pyrrhonota cytochrome ... 44 0.001 qb[AY005212.1] Podepiza whicii isolace 2 cytochrome b (cytb... gb[AY005211.1] Poospira whitii isolate i cytochrome b (cytb.... 9.991 qb|AF187122 1|AF187122 Cryptotermes tropicalis cytochrome 5 ... qb|AF187120 1|AF187120 Cryptotermes secundus cytochrome b | ... a.aat a.aat qb[AF[87]19.1[AF[87]18 Cryptotermes primus isolate 2 cytoch... 0.001 Cryptotermes primus isolate i cytoch ... 901AF183117.11AF183117 901AF183115.11AF183115 Cryptotermes dudlyl cytochrome b (Cy... 0.001 44 0.991 gbiAF112149 LIAF112149 Ovie canadensis cytochrome b gene. p ... 0.001 Ovie canadensis canadensis cytochrom. ... GDIARLIZILIZ LIARLIZILIZ Ovie canadenate network cytochrome b . 0.991 golafillig LLAFILLIS 44 0.001 901AF291779.11AF291779

gb[AF081989.1]AF081989	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081988.1 AF081988	Vireo cassinii cassinii specimen-vou	44	0.001
qb AF081987.1 AF081987	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081986.1 AF081986	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081985.1 AF081985	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081984.1 AF081984	Vireo cassinii cassinii specimen-vou	44	0.001
Gb AF081983.1 AF081981	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081982.1 AF081982	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081981.1 AF081981	Vireo cassinii cassinii specimen-vou	44	0.001
95 AF081980 . 1 AF081980	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081979.1 AF081979	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081978.1 AF081978	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081977.1 AF081977	Vireo cassinii cassinii specimen-vou	44	0.001
95 AF081976.1 AF081976	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081975.1 AF081975	Vireo cassinii cassinii specimen-vou	44	
gb AF081974 . 1 AF081974	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081973.1 AF081973	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081972.1 AF081972	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081971.1 AF081971	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081970.1 AF081970	Vireo solitarius alticola country US	44	0.001
gb AF081969.1 AF081969	Vireo solitarius alticola country US	44	0.001
gb AF081968.1 AF081968	Vireo solitarius alticola country US	44	0.001
gb AF081967.1 AF081967	Vireo solitarius alticola country US	44	0.001
gb AF081966.1 AF081966	Vireo solitarius solitarius specimen Vireo solitarius solitarius specimen	44	0.001
gb AF081965.1 AF081965	Vireo solitarius solitarius specimen	44	0.001
gb AF081964.1 AF081964	Vireo flavifrons specimen-voucher LS	44	0.001
gb AF081962.1 AF081962	Vireo flavifrons specimen-voucher LS	44	0.001
gb AF081961.1 AF081961 gb AF081960.1 AF081960	Vireo leucophrys leucophrys specimen	44	0.001
gb AF081959.1 AF081959	Vireolanius leucotis leucotis cytoch	44	0.001
gb AF112405.2 AF112405	Barbus anoplus cytochrome b (cytb) g	44	0.001
gb AF144317.1 AF144317	Amphibrion ocellaris isolate 3 haplo	44	0.001
gb AF144316.1 AF144316	Amphintion ocellaris haplotype 30Hll	44	0.001
GD AF144315.1 AF144315	Amphiprion ocellaris haplotype 3DH15	44	0.001
gb AF144314.1 AF144314	Amphiprion ocellaris isolate 2 haplo	44	0.001
gb AF144313.1 AF144313	Amphiprion ocellaris isolate 1 haplo	44	0.001
gb AF144312.1 AF144312	Amphiprion ocellaris haplotype 3DH12 Amphiprion ocellaris haplotype 3DH1	44	0.001
gb AF144311 . 1 AF144311	Amphiprion ocellaris isolate 2 haplo	44	0.001
gb AF144310.1 AF144310 gb AF144309.1 AF144309	Amphiprion ocellaris isolate 1 haplo	44	0.001
FINC 001567 1 Bos t	auria mirochondrion, complete genome	44	0.001
gb AF212124.1 AF212124	annija achwartzi cytochrome b gene,	44	0.001
95 AF182706 . 1 AF182706	phanitreron amethystina cytochrome b:	44	0.001
gb AF010406.1 AF010406	Ovis aries complete mitochondrial ge	44	0.001
gb AF096452.1 AF096452	Platysteira cyanea cytochrome b gene	44	0.001
gb AF283619.1 AF283619	Elaphe obsoleta LSUMZJ9162 cytochrom Elaphe obsoleta LSUMZ H15896 cytochr	44	0.001
95 AF283618.1 AF283618	Elaphe obsoleta LSUMZ H14782 cytochr	44	0.001
95 AFZ81608.1 AFZ81608 95 AFZ81602.1 AFZ81602		44	0.001
95 AF310069 . L AF310069	Flaenia martinica cytochrome b gene,	44	0.001
95 AF146616.1 AF146616	Actophilornis africanus cytochrome b	44	0.001
gb AF271410.1 AF271410	Galago moholi cycochrome b (cyc b) g	44	0.001
gb AF290139.1 AF290139	Peucedramus taeniatus cytochrome b (44	0.001
	pacos mitochondrion, complete genome Microtus ochrogaster cytochrome b ge	44	a.aal
qb AF163901.1 AF163901 qb AF119263.1 AF119263	Myonus achisticolor cytochrome b gen	44	0.001
gb AF119259.1 AF119259	symptomya borealis cytochrome b gen	44	0.001
95 AF288454 . L AF288454	Nycrareutes procyonoides koreensis C	44	0.001 0.001
qb AF153895.1 AF163895	Microrus gradalis cytochrome 8 (cyt8	44	0.001
gb AF123649.1 AF123649	Machaeropterus regulus ecriolatus cy Machaeropterus pyrocephalus cyrochro	4.1	0.00L
qb AF121647.1 AF121647	Kenopipo atronitena cytochrome b gen	44	0.001
96 AF121645.1 AF121645 96 AF121645.1 AF121645	pines fascilcauda cytochrome b gene	44	100.0
96 AF123634. 1 AF123634	purndamia acutatua cytochrome b gene	44	0.00L
qb AF123632.1 AF123532	Caphalonterus ornatus cytochrome b g	41	0.00L
90 AF121528 . 1 AF121529	Turdampella cryptolophua cytochrome Porphyrolaema porphyrolaema cytochro	_ 1	0.001
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95 AF127201.1 AF127201	lyrmothera campanisona cytochrome b	44	0.001
95 AF127192.1 AF127192	rallaria ruficapilla cytochrome b g	44	0.001
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95 AF127189.1 AF127189	dericornis frontalis cytochrome b ge	44	0.001
95 AF197849.1 AF197849 S	SELICOLUIS LICULALIS CYCOCULOUS - 3001	44	0.001
gb AF197847.1 AF197847	ardalotus striatus cytochrome b gen	44	0.001
ref NC 000889.1 Hippopo	camus amphibius mitochondrion, comp	44	0.001
ref NC 002079.1 Carassi	us auratus mitochondrion, complete	44	0.001
FINC 001794 11 Macropu	is robustus mitachandrion, complete		0.001
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115701612 1 AF201612 S	tromatorhique sp. CU79703 cyctchrome	44	0.001
125007031 1 A5097931 A	mphinrion clarkii cytochrome b gene	44	100.0
95 AF097927.1 AF097927 A	umphiprion ocellaris cytochrome b ge	44	0.001
GB AFU9/92/. ITAEU//92/	urus mitochondrion, complete genome	44	0.001
dp 101344.1 BOAMI BOS CO	palone spinifera isolate TXsc cytoc	44	0.001
	palone spinifera isolate TXki cytoc	44	0.001
	palone spinifera isolate TXcc cytoc	44	0.001
	palone spinifera isolate NMrg cytoc	44	0.001
	etrochelidon rufocollaris isolate E	44	0.001
	etrochelicon fulocollaris isolate E	44	0.001
	etrochelidon rufocollaris isolate E	44	0.001
gb U89187.1 MMU89187 Mon	notus mexicanus cytochrome b (cytb)	44	0.001
gb AF193833.1 AF193833 B	otaurus lentiginosus cytochrome b g		0.001
1 m 1 0 2 0 2 2 2 1 1 m 1 9 3 8 2 2 2	rdea alba cycochrome b gene, partia	44	0.001
- 1 - 21 02 02 1 1 B 21 93 821 B	rdea herodias cytochrome b gene, pa	44	0.001
1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	arabaja multifasciata cytochrome b	44	0.001
14 521 7025 1 1 A 521 7835 N	aja kaouthia cytochrome b gene, com	44	0.001
- 1 - 221 7224 7 BE217934 F	aricauda colubrina cytochrome b gen	44	
· 1	alliophia japonicus cytochrome b ge	44	0.001
1 1 1 5 F217923 M	icarnides euryxanthus cytochrome b	44	0.001
: 1	medalia coronata cytochrome b gene	44	0.001
1 1 221 707 E 1 3 E21 7815 B	ustrelans superbus cytochrome b gen	44	0.001
·	aranura humeralis specimen-voucher	44	0.001
114=00000 1 1 3=200078 E	www.arra isolate 62 cytochrome b g	44	0.001
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: 1. TOFO104 118 F059104 M	armarnarea accustifostris cytochro	44	0.001
: 1====== T 1 1 E E 1 1 T	onhonerra specularoides cytochrome	44	0.001
1117050054 1135059054 B	macoperra brasiliensis cytochrome D	44	0.001
1 1 22 02 C16 1 1 3 21 92 64 6 1	innocamous barbouri haplotype PH.22	44	0.001
1 1 2 2 4 2 4 4 5 1 3 2 1 4 2 5 4 5	innocambus barbouri haplotype PH.13	44	0.001
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: 1 - 2 : COC1 2 1 NE1 60613 C	riceromys emini Cemi531 cytochrome	44	0.001
: 1-51 COC12 1 1251 COC12 C	riceromys emini Cemis30 cytochrome	44	0.001
·	ricetomys emini Cemi637 cytochrome	44	0.001
· 1	ricetomys emini Cemi636 cytochrome	- 44	0.001
1 1 CO COA 1 3 E 1 CO COA C	alomyscus bailwardi Cbal576 cytochr	44	0.001
gb AF160560.1 AF160560 E	liurus majori Emaj642 cycochrome b	44	0.001
gb AF160559.1 AF160559 E	liurus majori Emaj641 cytochrome b	44	0.001
gb AF160558 . 1 AF160558 E	liurus majori Emaj639 cytochrome b	44	0.001
gb AF160557.1 AF160557 E	liurus majori Emaj638 cytochrome b	44	0.001
95 AF160555 . 1 AF160555 E	liurus majori Emaj614 cytochrome b liurus majori Emaj617 cytochrome b	44	0.001
	liurus majori Emajori cycochrome b	44	0.001
	liurus majori Emajiii cycochrome b	44	0.001
	liurus majori Emajosi cytochrome b	4.4	0.001
	liurus majori Emaj443 cycochrome b	44	0.001
	liurus majori Emaj444 cytochrome b	44	0.001
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-1125036286 1125036286 O	mor leucosta cytochrome b (cytb) ge	44	0.001
135076283 1145016281 A	arilone cervicapra cytochrome b (cy	44	a.aar
-6125036281 1125036281 A	oridorcas macsupialis cycochrome b	4.4	0.001
95 AF035278.L AF016278 T	racelaphus of/x cytochrome b (cytb)	4.4	0.001
LARGIETTE ILARGIETTE T	radelaphus eucyceros cytochrome b (44	0.001
qb AF0]5274 1 Tetraceru	a quadricomia cytochrome b (cytb)	44	0.001
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	icroryzomys minutus cytochrome 8 (c hipidomys nicela cytochrome 8 (cyts	44	0.001
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gb AF084074.1 AF084074 Lage	enorhynchus albirostris cytochrom	44	0.001
gb AF090750.1 AF090750 Gob	o gobio balcanicus cytochrome b	44	0.001
95 AF 0 90 7 30 . 1 1 1 2 1 5 7 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	mophilus columbianus columbianus	44	0.001
gb AF157939.1 AF157939 Spe	mophilus columbianus columbianus	44	0.001
gb AF157917.1 AF157917 Spen	mophilus washingtoni isolate 589	44	0.001
95 AF157936.1 AF157936 Spen	mophilus washingtoni isolate S88		0.001
95 AF157915.1 AF157915 Spen	mophilus richardsoni isolate S63	44	a.aal
Chings 57914 1 AF157914 Sper	monhilus richardsoni isolate 562	44	
182157917 1 AF157917 Sper	monhilus undulatus isolate S60 C	44	0.001
gb AF157906.1 AF157906 Spe	mophilus undulatus isolate SSS C	44	0.001
	mophilus elegans elegans isolate	44	100.0
	mophilus elegans elegans isoluenia	44	0.001
	mophilus columbianus columbianus	44	0.001
gb AF157859.1 AF157859 Spen	mophilus citellus isolate S118 c		0.001
- Lacistosa 1 AFT 57858 Sper	mophilus citellus isolate S117 C	44	
135157939 1 135157839 Sper	monhilus elegans elegans isolate	44	0.001
-blaco20497 118F030497 Croc	idura brunnea cytochrome b (cyt	44	0.001
gb U03541.2 LAU03541 Lenoxi	is apicalis cytochrome b gene, pa	44	0.001
	s appendiculatus cytochrome b (c	44	0.001
	ocichla tuba cytochrome b (cytb)	44	0.001
	ocienia tuna cycocinome o (cyco)	44	0.001
	ocentrus sajica cytochrome b (cy	44	0.001
	hyris whiteheadi cytochrome b ge		0.001
-6125094621 1145094621 Emiz	ia lepida cytochrome b gene, par	44	0.001
125094618 1 125094618 HVD6	rgerus atriceps cytochrome b gen	44	
	colarctos cinereus cytochrome b	44	0.001
13 21 5 9 5 9 7 1 1 4 5 1 5 8 5 9 7 Georg	wa burgarius ozarkensis cytochro	44	0.001
gb AF158694.1 AF158694 George	ys bursarius majusculus cycochro	44	0.001
	ys bursarius bursarius cytochrom	44	0.001
	ys bursarius missouriensis cytoc	44	0.001
	mophilus citellus cytochrome b (44	0.001
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	iciops gliroides cytochrome b se	44	0.001
	atus ursinus cytochrome b gene,	44	0.001
gb AF022065.1 Tragelaphus	euryceros cytochrome b (cytb) se		0.001
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-blacksans 1 Apridoress n	argunialis cytochrome b (cyto) 9	44	0.001
	ochaetes onou cytochrome o (cyto	44	0.001
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-Litteggaa TitTUEGRAA Lichar	ura trivizgata cytochrome b (cyt	44	0.001
12 21 431 93 1 A 21 431 93 Frit	enhelus sp. cytochrome b (cytb)	44	0.001
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gb AF081052.1 AF081052 Eule	mur rubriventer cytochrome b (cy	44	0.001
13 -001049 T 1 A -001049 Fule	mur macaco macaco cytochrome b (44	0.001
12 TO 23 CAR 1 A FOR 3 DAR FULL	mur fulvus albifrons cytochrome	44	0.001
	nia longicauda cytochrome b gene	44	0.001
- - TO 10067 1 U33 T10067 W	proporamus amphibius complete mi	44	0.001
Littlesos 1 LCT 1176506 Chlam	dera lauterbachii cytochrome b g	44	0.001
Luncena 1 CC176504 Chlama	dera cerviniventris cytochrome b	44	0.001
LITTEENE ILASITTESNE Ambluc	rnia subalaris cytochrome b gene	44	0.001
- Luncson Maggirsson Aschbo	idia naquensis cytochrome b gene	44	0.001
LUTECOR TIATUTESOR Ambive	rnia inornatus cytochrome b gene	44	100.0
145014969 11A5034969 Copp	ochaetes taurinus cytochrome b g	44	0.001
12 FOS1876 1 AFOS1876 Rhod	eus ocellatus cytochrome b (cytb	44	0.001
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qb S73150.1 S73150 cytochrome b (Spermophilus richardsonii=		100.0
qb AF012235.1 AF012235 Cryptomys hottentotus natalensis cyt		0.001
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Thirty 7062 1 PTU 7868 Rudorcas taxicolor taxicolor cytochrom		0.001
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gb/U17860 1/ODU17860 Ovis dalli cytochrome b gene, mitochon		0.001
gb/U17859.1/OCU17859 Ovis canadensis cytochrome b gene, mit		0.001
emb AJ010556.1 ASP010556 Acomys apinosissimus mitochondi latt.		0.001
gb AF034736.1 AF034736 Capra falconeri cytochrome b (cytb) gb AF034730.1 AF034730 Ovis aries cytochrome b (cytb) gene,		0.001
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gb AF034727.1 Ovis ammon darwini cytochrome b (cyto) gene, gb AF034724.1 AF034724 Pantholops hodgsoni cytochrome b (cytochrome b)		0.001
Linearing like034722 Adday pasomaculatus cytochrome b (Cy		0.001
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gb L29055.1 SHPMTDLOOP Sheep mitochondrial cytochrome b (Cy		0.001
gb AF082047.1 AF082047 Coccyzus americanus cycochrome b gen		0.001
gb AF038286.1 AF038286 Antechinus minimus cytochrome b gene gb AF038284.1 AF038284 Antechinus swainsonii cytochrome b g	44 (0.001
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gb AF059093.1 AF059093 Anas undulata cytochrome b gene, par gb AF059092.1 AF059092 Anas superciliosa rogersi cytochrome		0.001
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gb AF059078 1 AF059078 Anas laysanensis cytochrome b gene,	44 (0.001
gb/AF052240.1/AF052240 Anairetes flavirostris cytochiome 5		0.001
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db AF028180.1 AF028180 Urocyon cinereoargenteus cytochrome		0.001
gb AF028178.1 AF028178 Pseudalopex sechurae cytochrome b (C		0.001
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i broads a lastworker Annachinus swainsonii cytochrome b Se		0.001
timated illastifatet apreching maso cytochrome b gene, mit		0.001
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gb U07590.11PMU07590 Planigale maculata mitochondrion cytoc		0.001
emb AJ004326.1 PTAJ4326 Phylloscopus trochilus mitochondria gb AF020255.1 AF020255 Cyclura nubila cytochrome b (cytb) g		0.001
gb AF020255.1 AF020255 Cyclura nubila cytochrome b (cyto) g emb Y19184.1 L2A19184 Lama pacos complete mitochondrial genome		0.001
transca 11 Amphilophus cirrinellum cytochrome b (cytb) 95		0.001
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qb U88858.1 Thorichthys cf. aureum cycochrome b (cych) gen		0.00L
gb U88857.1 Herichthys labridens cytochrome b (cytb) gene gb U88856.1 Herichthys carpintis cytochrome b (cytb) gene	44 (0.001
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qb[U81356.1]CLU81356 Chelodina longicollia cyconrome b gen		0.001
db U77334.1 LUU75354 Leptomyrmex unicolor cytochrome b gene db U77332.1 CCU77332 Gymnorhinus cyanocephala cytochrome-b	44 (0.001
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emb AJ222680.1 TSCYTQB Tragelaphus spekil mitochondrial cyt.		0.001
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gb/U15718.1/RSU15718 Ramphocelus sanguinolentus cytochrome gb/L11905.1/CGYMTCYTBD Cratogeomys gymnurus mitochondrial c	44	0.001
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. Lynner 1 ler Cyre & longirostris cytochrome b gene (compl	44	0.001
gb U46771.1 ACU46771 Anthus campestris cytochrome b gene, m	44	0.001
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emb X74256.1 MIPVCYT3 P. violaceus mitochondrion gene for Cy	44	0.001
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db1 084202.1 COTMICEB Capra falconeri mitochondrial DNA for db1 084202.1 COTMICEB Capra falconeri mitochondrial DNA for db1 082821.1 082821 Bubalus bubalis mitochondrial DNA for c	4.1	0.001
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db1[082889.1[082882] Bos javanicus mitochondrial DNA for cyc	44	g.001
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gb AF027324.1 Akodon olivaceus canescens museum canalog pu	40	0.021
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gb[AF027314.1] Akodon olivaceus beatus museum catalog museum	40	0.021
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gb AF027312.11 Akodon olivaceus beatus museum caralog E	40	0.021
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gb AF324034.1 AF324034 Phyllobates aurotaenia isolate Quebt	40	0.021
ab/AF272619.1/AF272639 Clethrionomys gappers apeciment	40	0.021
gh AF272636.1 AF272636 Clethrionomys gappers specimen	40	0.021
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gb AF004572.1 AF004572 Arvicanthis niloticus cytochrome b (40	0.021
qb/AF088912.1/AF088932 Sminthopsis psammophila cytochrome b	40	0.021
qb U62697.1 ORUCYTB2 Oreopholus ruficollis cytochrome b (cy	40	0.021
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QD[U62661.1]CACIID2 CHAIAGLIUS AUSCIAIAS C/COCHE	3.8	0.084
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emb AJ004315.1 HCAJ4315 Hippolais caligata mitochondrial cy		

Alignments

tmpseq 0	1	cctcctagtttgttagggattgatcg	26
AF189111	797		772
U86834	858		833
AF123633	56		31
AF123617	104		79
AF127202	107		82
	107		82
AF127194			820
AF217828	845		844
AF160578	869		844
AF009931	869	• • • • • • • • • • • • • • • • • • • •	844
<u>AF091629</u>	869	• • • • • • • • • • • • • • • • • • • •	844
<u>AF034967</u>	869		844
<u>AF038290</u>	869	• • • • • • • • • • • • • • • • • • • •	
<u> 007577</u>	869		844
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AJ222681	869		844
M99464	869	• • • • • • • • • • • • • • • • • • • •	844
AJ225116	869		844
U25738	872		847
U25736	872		847
U15202	872		847
U15204	872		847
X56290	869		844
X56286	869		844
D88639	869		844
D82890	869		844
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AF123615	101		79
AF160603	866		844
U62687	179 ·		157
U62685	179		157
AF022071	866		844
AF022070	866		844
U83317	872		850
U37293	774		752
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U37291	774		752
AF082055	51		29
U72770	798	********	776
U07578	869		847
AF031908	187	• • • • • • • • • • • • • • • • • • • •	165
<u>AJ004231</u>	773	********	751 751
AJ004230	773	**************	751
AJ004229	773	••••••	751
AJ004232	773	* * * * * * * * * * * * * * * * * * * *	828
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<u>U90001</u>	773		75 L
<u>U63057</u> AB036404	173		151
AB036402	173		LSL
AB036400	173		151
AB036398	173		151
U19611	774		752
X92539	869		847
L08034	872		850
C04011	872		850
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AF974591	677	······································	736
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AF192133	797		772
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AF189118	797		772
AF189117	797		772
AF189116	797	gg.	772
AF112140	310	gg.	285
AF112139	310	· · · · · · · · · · · · · · · · · · ·	285
AF112138	310	gg	285
<u>AF081990</u>	872		847
AF081989	872		847
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AF081987	872		847
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AF081970	872		847
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AF081968	872		847
AF081967	872		847
<u>AF081966</u>	872		847 847
AF081965	872		847
AF081964	872 754		729
AF081962 AF081961	872		847
AF081960	872	gg	847
AF081959	872		847
<u> AFL12405</u>	869	c	844 136
AF144317	161 161	g	136
<u>AF144316</u> AF144315	161		136
AF144314	161	g	136
AF144313	161	g	136
AF144312	161	g	136
AF144111	161	g	136 136
AF144310	161 161	gg	136
AF144309 NC 001567	15382	gg	15357
AF212124	425		400
AF182706	739	a	714
AF010406	15027		15002 710
AF096452 AF283619	735 845		820
AF283618	845		820
AF283608	845		820
AF283602	845		820 745
AF310069	770 95	gg	70
AF146616 AF271410	95 869		844
AF290112	752	gg	727
NC 002504	15022	gg	14997
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	85		60
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Y10524	15052		15027
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U81356	791		766 427
U75354	452	· · · · · · · · · · · · · · · · · · ·	847
U77332 Z29573	872 15045		15020
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A1222583	669	••••••••••••••••••••••••••••••••••••••	844
M22456	069 067	•••••••	444
THE SAME		****	

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			844
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<u> U15205</u>	872	The state of the s	847
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			715
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AJ000427	740	a	715
	-	g	715
AJ000426	740		715
AJ000425	740	P	
AJ000418	740	a	715
AJ000417	740	a	715
	740	a	715
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AJ004793	770	t	745
AJ004792	770		
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	869	gg	844
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<u> </u>	869		844
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X72005	869	gg	844
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	869	gg	844
Y08813		g	844
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X60941	773		
X74255	872	gg	847
X56289	869	gg	844
V00654	15382	gg	15357
X60940	773		748
	869		844
X92530	774	g	749
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088635	869		844
088633	869		811
D88612			844
088610	869		844
	869		844
088628	669		844
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064202	869	· · · · · · · · · · · · · · · · · · ·	444
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<u>U10367</u>	773	· · · · · · · · · · · · · · · · · · ·	748
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<u> 296068</u> U76507	773		749
AF157466	791		772
AF157464	793		774
AF157463	793	* * * * * * * * * * * * * * * * * * * *	774
AY016019	93	• • • • • • • • • • • • • • • • • • • •	74 850
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AF027325	869		850
AF027324	869	*****	850 850
AF027323	869	•••••	850
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AF027320	869	*****	850
AF027319	869		850
AF027318	869	* * * * * * * * * * * * * * * * * * * *	850 850
AF027317	869		850
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AF027314	869	****	850
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AF155381	669 869		630
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AF264047	869		850
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AF206531	771	• • • • • • • • • • • • • • • • • • • •	• •
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AF004572	869		850
	869		850
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U62681	179		160
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<u>U62707</u>	179	gn	
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•			

Database: nt

Posted date: Mar 2, 2001 12:20 AM

Number of letters in database: 2,863,827,885 Number of sequences in database: 807,597

Lambda K H 1.37 0.711 1.31

Gapped

Lambda K H

X1: 6 (11.9 bits) X2: 15 (29.7 bits) S1: 12 (24.3 bits) S2: 16 (32.2 bits)

1.37 0.711 1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: S, Extension: 2
Number of Hits to DB: 19068
Number of Sequences: 807597
Number of extensions: 19068
Number of successful extensions: 7580
Number of sequences better than 10.0: 2441
length of query: 26
length of database: 2,863,827,885
effective HSP length: 17
effective length of query: 9
effective length of database: 2,850,098,736
effective search space: 25650888624
effective search space used: 25650888624
T: 0
A: 30

Table 12. The other animals belonging to distantly related species analyzed by our primers to demonstrate its universal nature

SN.	Name of the animal
	Indian black buck no.1
1.	
2.	Indian black buck no 2
3	sheep
4	pig
5	dog
6	chimpanzee (chimss)
7	human (humsk)
8	Hamster
9	crocodile nol
10	crocodile no2
11	turtle no l
12	turtle no2
13	mouse
14	varanus
15	Naga-naga snake
16	Indian elephant
17	hen
18	dugong
19	lizard
20	weaver bird no l
21	weaver bird no.2
22	buffalo no l
23	buffalo no 2

CLAIMS

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1 Universal primers named as 'mcb 398' and 'mcb 869' capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal of unknown origin at species and sub-species level, said primers, having the sequences:

primers name

Sequence (5'-3')

mcb 398

"TACCATGAGGACAAATATCATTCTG"

mcb 869

"CCTCCTAGTTTGTTAGGGATTGATCG

- 2. Primers as claimed in claim 1 wherein the fragment of mitochondrial cytochrome b gene is capable of significantly discriminating amongst various evolutionary lineages of different animal species.
 - 3. Primers as claimed in claim 1 wherein the fragment of mitochondrial cytochrome b gene is flanked by the highly conserved sequences amongst a vast range of animal species.
- 4. Primers as claimed in claim 1 wherein the fragment on mitochondrial cytochrome b gene which is polymorphic inter-specifically, but monomorphic at intra species sources.
 - 5. Primers as claimed in claim 1 wherein in Antilope cervicapra species, the sequences of the fragment mentioned under claim 1 are as follows:
- 20 Mitochondrial cytochrome b gene sequence (398-869 bp) of Antilope cervicapra:
 "taccatgaggacaaatatetttttgaggagcaacagtcatcaccaatetcetttcagcaatcccatacateggtacaaacctag
 tagaatgaatetgaggagggttetcagtagataaagcaaccettacccgatttttcgccttccactttatcctcccatttatcattgc
 agcccttaccatagtacacctactgtttctccacgaaacaggatccaacaaccccacaggaatctcatcagacgcagacaaa
 attccattccacccctactacactatcaaagatatcctaggagctctactattaattttaaccctcatgettctagtcctattcaccc
 ggacctgcttggagacccagacaactatacaccagcaaacccacttaatacacccccacatatcaagcccgaatgatacttc
 ctatttgcatacgcaatcctccgatcaattcctaacaaactaggagg"
 - 6. A method for the identification of the animal from a biological sample, said method comprising the steps of:
 - a) isolating and amplifying the DNA from the biological sample to be tested using the primers as claimed in claim 1,
 - b) sequencing the amplified products,
 - c) blasting the sequence resolved in step (b) against mito database of National Centre for Biotechnology Information (NCBI) using BLAST program and determining the most likely family of the animal source of the biological sample,

- d) blasting the sequence resolved in step (b) against non-redundant (nr) database of National Centre for Biotechnology Information (NCBI) using BLAST program and determining the most likely genus, species or more precisely the sub-species of the animal source of the biological sample,
- e) identifying the most significant alignment of the sequence resolved with cytochrome b gene sequence of the animal identified in steps (c) and (d) respectively and selection of these animals as 'reference animals' for further studies,

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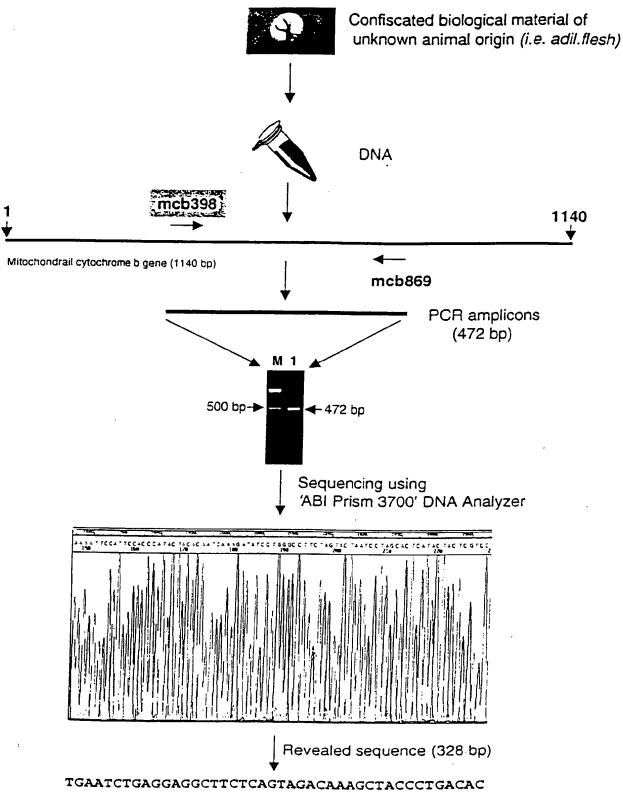
- f) isolating and amplifying and sequencing the DNA sequences from the reference animal on both strands in triplicate using the primers as claimed in claim 1,
- g) aligning the sequences obtained using CLUSTRAL program and identifying the variable sites amongst the animals analyzed,
- h) comparing the nucleotide sequences pair-wise to determine the variation among the animals resolved and identifying the nucleotide sequence to which the DNA sequence of the biological sample bears maximum similarity as the source animal of the biological sample.
- 7. A method as claimed in claim 6 wherein the universal PCR protocol works universally with the DNA template of any unknown animal origin and the universal primers mentioned under column 4.
- 8. A method as claimed in claim 6 wherein the Amplification reactions should be carried out in 20 μl reaction volume containing approximately 20 ηg of template DNA, 100μm each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl₂, 0.5 unit of Ampli*Taq* Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed should be: an initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step at 35th cycles should be held for 10 min.
- 9. A method as claimed in claim 6 wherein the method enables identification of species of analyzed material (i.e. the DNA isolated from confiscated animal remain of unknown origin) using the public databases such as GenBank, NCBI etc.
- 10. A method as claimed in claim 6 wherein the method is used for animal identification to establish the crime with the criminal beyond a reasonably doubt.
- 11. A method as claimed in claim 6 wherein the method is used to establish the identity of

- biological materials such as skin, homs etc confiscated from animal poachers, if it is that of an endangered species.
- 12. A method as claimed in claim 6 wherein the method is used for establishment of the identity of confiscated animal parts and products of endangered animal species for the purpose of production of molecular evidence of animal hunting and related crime in the court of law, so that the human violation of the wildlife resources could be controlled.

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- 13. A method as claimed in claim 6 wherein the method is used to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented.
- 10 14. A method as claimed in claim 6 wherein the method is used for animal identification to detect the adulteration of animal meat in food products for the purpose of food fortification, by the food fortification agencies.
 - 15. A method as claimed in claim 6 wherein the method is used to provide a universal technique for detection of the origin of blood or blood stains etc collected from the scene of crime related to offences such as murder, rape etc, in order to establish the origin of blood found at scene of crime when it sounds as if criminals have wontedly spread the blood of an animal at the scene of crime, to confuse the crime investigation agencies and forensic scientists with human blood.
- 16. A method as claimed in claim 6 wherein the method is used so that it can be converted to a (a) <u>COMMERCIAL 'MOLECUALR KIT'</u> and (b) <u>'DNA CHIPS'</u> based applications for wildlife identification in forensics.



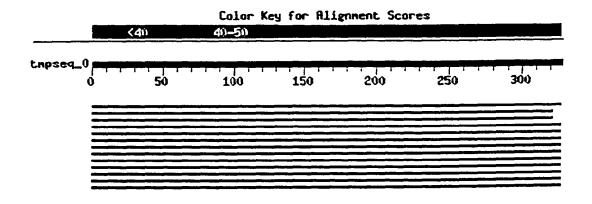
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ACTAATCCTAGCACTCATACTACTCGTCCTATTCTCACCAGAC
CTGTTAGGAGACCCCGATAACTACATCCCTGCCAACCCTCTAA
ATACCCCTCCCCATATCAAGCCTGAAT

Figure 1 a

Sequence of cytochrome b gene (328 bp) revealed from biological material of unknown origin i.e. 'adil.flesh' using primers 'mcb398' and 'mcb869'

Homology search in 'nr' database using 'BLAST'

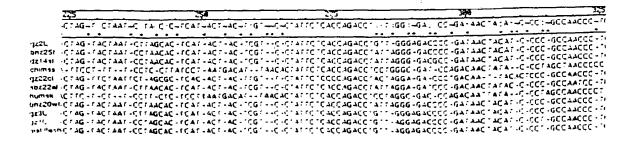
http://www.ncbi.nlm.nih.gov/BLAST/



Sequences producing significant alignments:	Score (bits)	E Value
gb AY005809.1 <i>Panthera pardus</i> cytochrome b gene, partial c gb AF053054.1 AF053054 <i>Panthera tigris sumatrae</i> isolate Su1 gb AF053053.1 AF053053 <i>Panthera tigris tigris</i> isolate B7 mi gb AF053050.1 AF053050 <i>Panthera tigris corbetti</i> isolate C2 gb AF053049.1 AF053049 <i>Panthera tigris corbetti</i> isolate C1		e-170 e-147 e-147 e-132 e-132

Selection of reference animals based on above information and further analysis using primers 'mcb398' and 'mcb869'

Multiple sequence alignments using 'Autoassembler'



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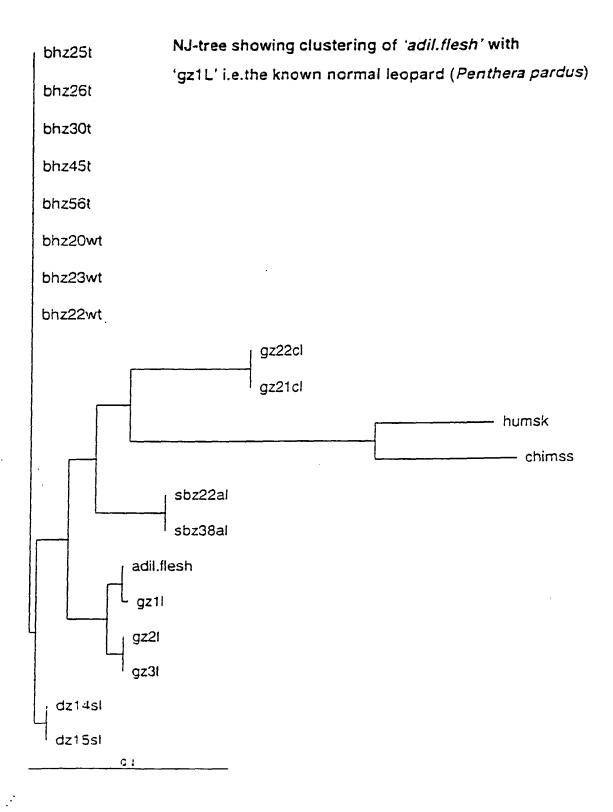


Figure 1c

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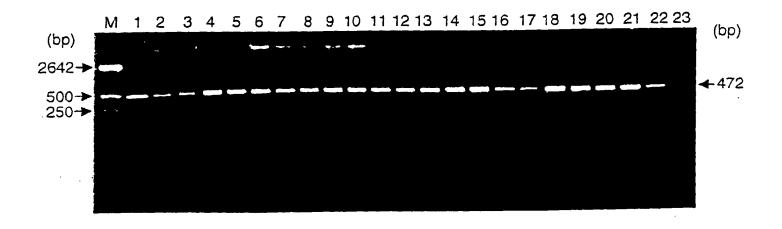


Figure 2

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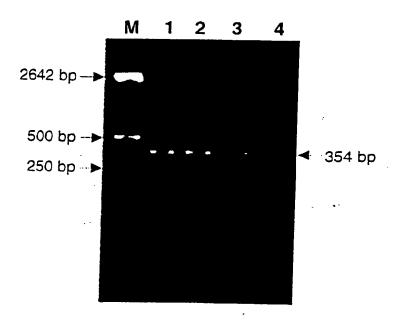


Figure 3

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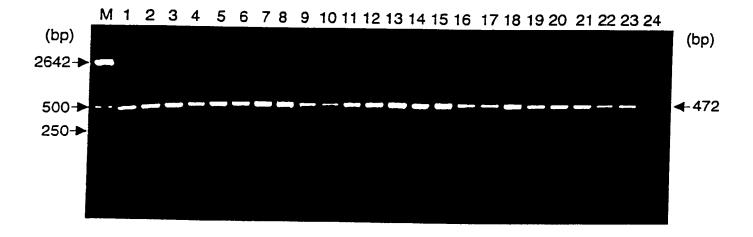


Figure 4

INTERNATIONAL SEARCH REPORT

PC 1/11N 01/00055

A. CLASSIFICATION OF SUBJECT MATTER IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols) IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, EPO-Internal, EMBL, WPI Data, PAJ, MEDLINE, EMBASE

Category °	Cilation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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Y	WO 92 05277 A (DAVIDSON WILLIAM SCOTT;BARTLETT SYLVIA ERNESTINE (CA)) 2 April 1992 (1992-04-02) the whole document/	1-16

X Further documents are listed in the continuation of box C.	X Patent family members are listed in annex.
Special categories of cited documents: A* document defining the general state of the art which is not considered to be of particular relevance E* earlier document but published on or after the international filing date L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) O* document referring to an oral disclosure, use, exhibition or other means P* document published prior to the international filing date but later than the priority date claimed	 *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art. *&* document member of the same patent family
Date of the actual completion of the international search 28 February 2002	Date of mailing of the international search report 12/03/2002
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Authorized officer Hagenmaier, S

INTERNATIONAL SEARCH REPORT

Internal Application No

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT Category © Citation of document, with indication, where appropriate, of the relevant passages Relevant to claim No.					
Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.				
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